

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 210734

TO: Manjunath N Rao

Location: REM-2A01/2C70

Art Unit: 1652

Wednesday, December 20, 2006 Case Serial Number: 10/616101

From: Usha Shrestha

Location: Biotech-Chem Library

REM-1A64

Phone: (571)272-3519

Usha.shrestha@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Usha Shrestha
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-3519

Specialist Library

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12-759 STIC-Biotech/ChemLib

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To:

Sent:

Chan, Christina

Monday; December 18, 2006 8:56 AM Rao, Manjunath N.; STIC-Biotech/ChemLib

Subject:

RE: REquest for RUSH segeunce search for case No. 10/616101

Please wish. Thanks Chais

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 (571) - 272 - 0841Remsen, 3E89

----Original Message----

From: Rao, Manjunath N.

Sent: Friday, December 15, 2006 2:23 PM

To: Chan, Christina

Subject: REquest for RUSH sequence search for case No. 10/616101

Hello Christina,

Please authorize the search request below as RUSH. The reason being this is an amended case and applicants have now included SEQ ID NO for the claimed polypeptides.

Many Thanks -Manjunath

Manjunath N. Rao, Ph.D.

Primary Examiner, Art Unit 1652

Room 2A01, Remsen Bldg.

United States Patent and Trademark Office

400, Dulany St.

Alexandria, VA 22314 Phone: 571-272-0939

Fax: 571-273-0939

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From: Manjunath N. Rao		
Art Unit 1652, Room 2A01		
Mail Box in Room 2C70		
Phone: 272-0939	•	
Date: 12-15-06		
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Online Time:	Inventor: Litigation:	SEQUENCE SYSTEM:
		WWW/Internet:
		Other (Specify):

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

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Searched:

Database

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                                               GTCTGTGGAGGAAGGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGG
                                       TGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTATG
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Luo,Y., Chan,E., Xu,X., Huang,B. and Ossovskaya,V.
Tankyrase H, compositions involved in the cell cyc
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Patent: US 6887675-A 2 03-MAY-2005;
Rigel Pharmaceuticals, Inc.; South San Francisco,
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Qy 3643 GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG 3702 bb 3662 GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG 3721 Qy 3703 ATAAATAGTTATTTTAAGAAACTTACTCGACTGAACCTAAAATCATCAAAGCAGCAGTGG 3762 bb 3722 ATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTGG 3763 CQy 3763 CCTCTACGTTTACTCCTTTGCTGAAAAAAAAA 3797 Db 3782 CCTCTAACGTTTTACTCCTTTGCTGAAAAAAAAA 3816	RESULT 5 AR361486 LOCUS LOCUS DEPINITION Sequence 5 from patent US 6599728. AR361486.1 G1:33769334 AR361486.1 G1:33769334 KEYWORDS SOURCE Unknown. Unclassified. Unclassif	Query Match 89.2%; Score 3388.8; DB 2; Length 4275; Best Local Similarity 99.9%; Pred. No. 0; Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 403 AGGTTTTGGGGGGAAGGTGTTGAATTGGTTCAGATGGTGCAAGTGTCCAAGC 540 Bb 481 AGGTGATGATGGGGGAAGGTGGTTGAATTGGTTCAGATGGTCCAAGC 540 Bb 482 AGGTGATGATGGGGGGCTTATTGGTTGAATTGGTTGGAAGT 522 Bb 541 AGGTGATGATGGGGGCCTTATTGCTCTTTAGATGGTGATGGTGAAGT 600 CO 523 AGTCATTGCGGGGCCTTATTGCTCTTTAGATGGTGTTTTGGTGATGTGGTGAAGT 600 CO 523 AGTCATTCCCTTTTGCGAAGCCCCAATGGTGGAATTTATC CO 523 AGTCATTCCTTTTGCGAACTGCAATTAAGGAACTCCTGAAATTATTGCATTGGAATTATTAC CO 601 AGTCATTCCCTTTTGCGAACTGCAATTAAGAATTAAGAACTCTGAAATTAAGAATTAAGAACTGCAATTAAGAATTAAGAACTATTATGCATTTAGAATTAACAATTAAGAATTAAATTAAGAAAATTAAGAAAATTAAAGAATTAAATAAGAAATTAAAGAAAAATTAAATAAAAATTAAAGAAAAAA

TGCTAAAGGTAAAGGAGGCCTTGTACCTTTGCACAATGC 1902 FINITEGETCATTATGAAGTAACTGAACTTTTGGTCAAGGA 1080 RACACCTITACATGAAGCAGCAGCAAAAGGAAAATATGA 2022 TATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCA 1002 AATGAAATGTACAGCAACTCCTCCAAGAGGGTATCTC SGACTICIGGCAATICACTCCTCTTCATGAGGCAGCTIC TCTCTTCTCTTAAGTTATGGTGCAGACCAACACTGCT TCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG CAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT

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Chi,N.-W. and Lodish,H.F.
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                                        TGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTATG
                                                                                         GGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAAGAAAACCACAACCATGCCAATGA
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      CACACCTITGCACGAAGCAGCCCAAAAGGGACGAACAACACACTITGIGCTITGTIGCTAGC
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/map="10q23.1"
/note="STS WI-16054"
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3569 TTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCAC 3628
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1 (bases 1 to 3815)

Lyons, Lyons, D.K., Ye, Z.S., Sanderson, G.M.,

Eyre, H.J., Sutherland, G.R. and Daly, R.J.

Identification of a novel human tankyrase through its interaction with the adaptor protein Grb14

J. Biol. Chem. 276 (20), 17172-17180 (2001)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Byre, H.J., Sutherland, G.R. and Daly, R.J.

Byre, H.J., Sutherland, G.R. and Daly, R.J.

Submitted (17-DEC-2000) Cancer Research, Garvan Institute of Medical Research, 384 Victoria St., Sydney, NSW 2010, Australia Location/Qualifiers

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Matches 3389; Conservative
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ò	1483 TAATGCTCT	NATIGECTICTICGATAATCTTIGGECAGACTTCTTACACAGAGCTGCATATTGTIGGECATCT 1542
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ò	1663 ATTAGGTAA	-
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q	1657 AACTGTAAA	CAACTGCAGAGACATTGAAGGGCGTCA
ර ර		ATTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT
Q Q	17 Grei	ATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT
ඊ සි	1843 ACAGCATGGAGCTG	
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ි සි	1903 AIGIICIIAIGGAC 	ATTALGAMOTIGCAGAACTICTICTICTIAAACATGGAGGAGTAATTAAAAAAAAAA
Š	1963 TGTAGCTGAT	ITTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAAGGAAAATATGA 2022
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ò	2263 AGCTGGTTAT	23
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
Tankyrase2 materials and methods
Patent: WO 0100849-A 100 04-JAN-2001;
ICOS CORPORATION (US)
LOCATION (US)
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AX062241.1 GI:12540142
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Mammalia, Butheria, Euarchontoglires; Primates, Catarrhini;
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Patent: WO 010849-A 106 04-JAN-2001;
ICOS CORPORATION (US)
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89.2%; Score 3387.2; DB 2; Length 4406;
Best Local Similarity 99.9%; Pred. No. 0;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
Tankyrase2 materials and methods
Patent: WO 0100849-A 134 04-JAN-2001;
ICOS CORPORATION (US)
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AX062275.
AX062275.1 GI:12540176
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Best Local Similarity
Matches 3389; Conserv
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Euarchontoglires, Primates, Catarrhini;
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Tankyrase2 materials and methods
Patent: WO 0100849-A 132 04-JAN-2001;
ICOS CORPORATION (US)
Location/Qualifiers
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//organism="Homo sapiens"
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Mammalia; Eutheria;
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Matches 3389; Conservative
                                                                                                                                                                   Hominidae; Homo.
                                                                                               Homo sapiens
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Unclassified.

1 (bases 1 to 5075)
3 Tang,Y.T., Goodrich,R.W., Asundi,V. and Drr Catheppin V.like polypeptides
L. Patent: US 6783969-A 556 31-AUG-2004;
Nuvelo, Inc.; Sunnyvale, CA
3 Location/Qualifiers
1 5075/
/organism="unknown"
/mol_type="genomic DNA"
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; Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 3389; Conservative
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14-DEC-2004

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AR578380 56075 bp DN Sequence 556 from patent US 6783969. AR578380

GI:56581176

AR578380.1 . Unknown. Unknown.

AR578380 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 13

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Homo sapiens tankyrase-like protein (TNKL) mRNA, complete cds.
AF264912
                                                       TITCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCAC 3582
                                                                                    TTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCAC 3629
                                                                                                                 TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACA 3642
                                                                                                                                            CAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTC 3522
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 5810)

Kulmov,A.N., Kuprash,D.V., Petrov,V.N., Vdovichenko,K.K.,
Scanlan,M.J., Jongeneel,C.V., Lagarkova,M.A. and Nedospasov,S.A.
Cloning and characterization of TNKL, a member of tankyrase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-MAY-2000) Laboratory of Molecular Immunology, A.N. Belozersky Institute of Physico-Chemical Biology, Moscow State University, Moscow 119899, Russia Location/Qualifiers
             CAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTC
                                                                                                                                                                         GGCTTATCCTGAGTATTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TNKL"
/note="a new member of tankyrase gene family; current
Unigene claster Hs.168491"
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2 (bases 1 to 5810)
Kuimov,A.N., Kuprash,D.V., Petrov,V.N., Vdovichenko,K.K.,
Kashkarova,U.A., Boitchenko,V.E., Nedospasov,S.A. and
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| organism="Homo sapiens"
| /mol_type="mRNA"
| /mol_type="mRNA"
| /mol_type="mRNA"
| /chromosome="10"
| /msp="log22-log24"
| /msue="log22-log44"
| /note="derived from clones MO-BC-203 and I203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="a new member of tankyrase family"
/codon_start=1
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/protein_id="AAG44694.1"
/db_xref="G1:12005976"
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QFTPLHEAASKRRVEVCSLLLSYGADPTLANCHNKSAIDLAPTPQLKERLAYEFKGHS
LLQAAREADVTRIKKGHISLERWNFKHPQTHETALHCAAASPYRKKQTCELLERGAN
LLLSYGCDPNI ISLOGFTALOMERAKVNALDNLGGTSLHRAAYCGHLQTCR
LLLSYGCDPNI ISLOGFTALOMERAKVNALDNLGGTSLHRAAYCGHLQTCR
LLLSYGCDPNI ISLOGFTALOMENWQDLLOGGISLGNSEADRQLLEAAKGGDVETV
KKLCTVQSYNCRDIEGRQSTPLHFAAGYNNVSVVEYLLQHGADVHAKOKGGIVPLHNA
CSYGHYEVAELLVKGGTDTQDLLROBALLDAAKKGCLLARVKLSSPDNVCRDTGROFFTV
GNTPPLLDLXXGGTDTDQDLLROBADNALDAAKKGCLLARVKLSSPDNVCRDTGREND
GNTPPLLDLXXGGTDTQDLLROBADNALDAAKKGCLLARVKLSSPDNVCRDTGREND
GNTPPLLSYNNLGVARSTLCALLLAHGADVNAQDDTLKNQGGTPLDLVSADDVSALLTAAM
PDSALPSCYKRQVLUKGVRSPCATADALSAGSSPSSPSSLSASASSLDNLSGSSFSELSSVVS
SGTBGASSLEKKEVPGVDPS ITQPKRNLGLEHLANDIFCRSAASSLDNLSGSFSEENS
GSTTRGASSLEKKEVPGVDPS ITQPKRNLGLEHLANDIFCRSEDNHAHREKLEK
HGSPFVNAITHKGPDERHAYIGGKGGGTIPLDVLVBEGFFGSVEEEM
GSTYRKERDGGGAGTIPLLAGGGGTIPLDVLVBEGFFGSVEEEM
GSTYRKERDGGGAGTIPLLKNGCKTRWERYTHRKEVSEEBHHFANRER
HGSPFVNAITHKGPDERHAYIGGKGGATYARESKSNGNGYTGGGTGCPPHKDRS
CYTCHRQLLFCRVTLGKSFCATYARESKSNGNGTALABERVITRGEG
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89.2%; Score 3387.2;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches
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/note="SHGC-53837"
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/note="WI-8339"
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/note="WI-16054"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	AAA91487 Aaa91487 Tankyrage	ABQ77066 Tankyrase	4	4 ADY97759 Human tan	AAA91488 Tankyrase		D ADH69415 Adh69415 Human tan	4 ADY97760 Human tar	AAC66825 Human tan	AAC85294 Human SPA	AAF63926 Auman tan	AAF63930 Human tar		AAF63952 Human tan		
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ALIGNMENTS

RESULT 1 AAA91487

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Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation; cell cycle protein; cell cycle associated disorder; cancer; gene mapping; chromosome mapping; gene therapy; vaccine; ds.
                                                                                                                                                      /+tag= a
/partial
/product= "TaHol"
/note= "Tankyrase homologue isotype 1; No start codon
given"
                                                        Tankyrase homologue isotype 1 coding sequence.
                                                                                                                                  Location/Qualifiers
BP.
                                                                                                                                                                                                                                                                                                               Huang B;
                                                                                                                                                                                                                                                                         99US-00427154.
                                                                                                                                                                                                                                                       25-OCT-2000; 2000WO-US041528.
AAA91487 standard; DNA; 3797
                                      (first entry)
                                                                                                                                                                                                                                                                                            (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                               Luo Y, Chan E, Xu X,
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P-PSDB; AAY97748.
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                  AAA91487;
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                             11X88X1X8X1X1111111111X8X6X1X1X1X1X8XX1X1X
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Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating

Adr14766 Nucleotid

6189 13 ADR14766 '

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18 3387.2

or preventing cell cycle associated disorders such as cancer

Claim 13; Fig 1; 63pp; English

This sequence encodes the Tankyrase homologue isotype 1 (TaHo-1) protein of the invention. The invention also relates to the TaHo-2 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo conding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also generation of anti-sense DNA and RNA, The coding sequences are also useful for the preparation of TaHo, for generating either transgenic and screening of therapeutically useful agents, in gene transgenic and screening of therapeutically useful agents, in gene therapy, as and screening of therapeutically useful agents, in gene therapy, as gene which encodes TaHo and for the genetic analysis of individuals with a screening of the TaHo proteins, and their coding sequences are useful in screening assays

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Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 0; AGACAAATATTAGCTGTGAGCAGATCTTTTTTTGTTGCTT Н 61 61 121 181 121 181 241 241 301 301 361 361 481 541 601 661 421 421 481 541 601

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d d	781	AATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGCAAGTGATGGCAGAAAGTC 840
ò	841	AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTACTGCA 900
qq	841	AACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTACTGCA 900
ò.	901	ACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGTACCATTACACAATGCCTG 960
QQ	901	ACATGGAGCTGATGCCATGCTAAAGATAAAGGTGATCTGGTACCATTACACAATGCCTG 960
δ,	961	TICITATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAAATGC 1020
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è	1081	AIGITCTCTTCTTAAGTTATGGTGCAGACCCAACACTGGTCCAATTGTCACAATAAAG 1140
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ò	1261	
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οp	1321	TGCATCTCCATATCCCAAAAGAAAGCAAATATGTGAACTGTTGCTAAGAAAAGGAGCAAA 1380
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qq	1441	TAATGATGTTGAAGTAGTGGAAACATGAAGGAAAGGTTAATGCTCTGGATAATCT 1500
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QΩ	1501	TGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATCTACAAACCTGCCGCCTACT 1560
ò	1561	61 CCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGAT 1620
qq	1561	CCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGAT 1620
è	1621	GGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTCATTAGGTAATTCAGAGGC 1680
qg	1621	~
ò	1691	AGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGAAACTGTAAAAAAACTGT 1740
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1801 TGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCTACAGCATGGAGCTGATGT 1860 	1861 GCATGCTAAAGATAAAGGGGCCTTGTACCACAATGCATGTTCTTATGGACATTA 1920 	TGAAGTTGCAGAACTTCTTGTTAAACATGGAGAGTAGTTAATGTAGCTGATTTATGGAA 	ATTTACACCTTTACATGAAGCAGCACAAAGGAAAATATGAAATTTGCAAACTTCTGCT	1981 ATTTACACCTITACATGAAGCAACAGCAAAATATGAAATTGCCAACTTCTGCT 2040 2041 CCAGCATGGTGCAGACCCTACCAAAAAAACAGGATGGAATACTCCTTTGGATCTTGT 2100 2041 CCAGCATGGTGCAGACCCTACCAAAAAAAAAGGGATGGAATAGAATACTCCTTTGGATCTTGT 2100	TAAAGATGGAGATACAGATCTGCTTAGGGGAGATGCGGCTTTGCTAGATGCTTGCT	Teccaacaacacticitaaccacactaactaacticicetectectaatataatte	2221 CCGCGATACCCCAAGGCAGACATTCAACACCTTTACATTTAGCAGCTGGTTATAATTT 2280 	2281 AGAAGTTGCAGAGTATTTGTTACAACACGGAGCTGATGTGAATGCCCAAGACGAAGGAGG 2340 	2341 ACTIAITCCTITACAIAATGCAGCATCTIACGGGCATGTAGATGTAGCAGCTCTACTAAT 2400 	2401 AAAGTATAATGCATGTGTCAATGCCACGGACAAATGGGCTTTCACACCTTTGCACGAAGC 2460	AGCCCAAAAGGGACGAACACAGCTTTGTGCTTTGTTGCTAGCCCATGGAGCTGACCGAC	2521 TCTTABABATCAGGAAGGACABACACCTTTAGATTTAGTTTCAGCGGATGATGATGTGGCG 2580 2521 TCTTABABATCAGGAAGGACAAACACCTTTAGATTTAGTTTCAGCGGATGATGATGACGC 2580	TCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCTTGTTACAAGCCTCAAGTGCT 	CAATGGTGTGAGAAGCCCAGGAGCCACTGCAGATGCTCTTCAGGTCCATCTAGCCCC	2641 CAATGGTGAGAAGCCCAGGAGCCACTGCAGATGCTCTCTTCAGGTCCATCTAGCCC 2700 2701 ATCAAGCCTTTCTGCAGCCAGCAGCTCTTGACAACTTATCTGGGAGTTTTTCAGAACTGTC 2760 2701 ATCAAGCCTTTCTGCAGCCAGCAGCTTGACAACTTATCTGGGAGTTTTTCAGAACTGTC 2760	2761 ITCAGTAGTTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTTTGGAGAAAAAGGAGGTTCC 2820 	2821 AGGAGTAGATTTTAGCATACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATGGA 2880	
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Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-1; TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour; cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
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bioactive agent screening; cancer; cytostatic; gene; human;
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                                          Huang B, Ossovskaya V;
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100.0%; Score 3797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches
                                                                                                                             Claim 10; SEQ ID NO 1; 75pp; English.
                                          Chan E, Xu X,
                     OSSOVSKAYA V.
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                                                               WPI; 2005-294737/30.
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421 CGTAGTTGAATATTTGCTTCAGAATGGTGCAAGTGCTCCAAGCACGTGATGATGGGGGGCCT 480 421 CGTAGTTGAATATTTGCTTCAGAATGGTGCAAGTGCTCCAAGCACGTGATGGAGGGGCCT 480 431 TATTCCTCTTCATAATGCATGCTCTTTTGGTCAGTGCTGAAGTAGTTCCTTTTGCG 540 431 TATTCCTCTTCATAATGCATGCTCTTTTTGGTCAGTGCTGAAGTAGTCCTTTTTTGCG 540 431 TATTCCTCTTCATAATGCATGCTCTTTTTGGTCAAGTAGTACTCCTTCCT	CCGGAAATGCTGCAAGCTGCACAAGAACTGAAGTTACTCGAATCAAGAAACACTCTCTCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-1 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the genetic disorders. The TaHo proteins, and their coding sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                     Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation; cell cycle protein; cell cycle associated disorder; cancer; gene mapping; chromosome mapping; gene therapy; vaccine; ds.
                                                         /note= "Tankyrase homologue isotype 2; No start codon given"
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1423 GGCATCTGAGAAAGCTCATAATGATGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT 1482	CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC 1	ATTAGGTAATTCAGAGGCAGACAACTGCTGGAAGCTGCAAAGGCTGGAGATGTCGAAAGCTGGAAATTCAGAGAGCTGGAAGCTGCAAAGGCTGGAGATGTCGAAAGCTGCAAAAAAAA	1783 GTCTACACCACTTCATTTTGCAGCTGTATAACAGAGTGTCCGTGGTGGAATATCTGCT 1842	1862 ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGAGGGGCCTTGTACCTTTGCACAATGC 1921 1903 AIGITCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA 1962 1922 AIGITCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA 1981 1922 AIGITCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTAAA 1981	TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGAAAGGAAATATGA	2023 ANTITICCARACTICICICCACCATGOTICCARACCCARACACACACACACACACACACACACACACA	2102 TACTCCTTTGGATCTTGTTAAAGATGGAGATATTCAAGATCTTGCTTAGGGGAGA 2161 2143 TGCAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTAGCCAAGAGATGTCTTC 2202 2143 TGCAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTAGCCAAGAGAAGTGTCTTC 2202 2151 THIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGACATTCAACACCTTTACATTTAGC 		TGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGA 	2383 TGTAGCAGCTCTACTAATAAAGTATAATGCATGTGTCAATGCCACGGACAATGGGGCTTT 2442 	2443 CACACTITGCACGAAGGCCCAAAGGGACGAACACACGCITIGICTITGITGCTAGC 2502 [
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Query Match 89.4%; Score 3393.4; DB 4; Length 3816; Best Local Similarity 99.9%; Pred: No. 0; 1; Indels 0; Gaps 0; Matches 3394; Conservative 0; Mismatches 1; 1; Indels 0; Gaps 0; 403 AGGTTTTGGCCGAAAGACGTAGTTGATATTTGCTTCAGAATGGTCCAAGTGCAAGGC 462 422 AGGTTTTGGCGGAAAGACGTAGTTGATATTTTCGTCAAATGGTCAAGCGAAGG 481 423 AGGTATTGGCGGGGCCTTATTCCTCTTCAAAATGGTCAAGCTGAAGTGTCAAGCTGAAGGCGAAGGCGTAGTTCAAAAAGACGTAGTTGAAAAAGACTAGTTGAAGAGTGTCATTTTTGGTCAAGCTGAAGGCGGGCCTTATTCCTCTTTTTTTT	482 ACGTGATGATGGGGGCCTTATTCCTCTTCATAATGCATGC		ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG	782 GAGTGGCAATGAAAAAATGATGGCTCTTACTCACACATTAAATGTCAACTGCCACGC 841 823 AAGTGATGGCAGAAAAGTCACTCCATTACATTGGCAGGATATAACAGAGATAAAAGTT 882 823 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGATATAACAGAGTAAAGAT 882	TGTACAGCTGTTACTGCAACATGGAGGTGATGTCCATGCTAAAGATAAAGGTGATCTGGT	accattacacaatgcctgttcttatggtcattatgaagtaactgaacttttggtcaagca 	1003 TGGTGCCTGTGTAATGCAATGGACTTGTGCCAATTCACTCCTTCATGAGGCAGCTTC 1062	1082 TAAGAACAGGGTTGAAGTATCTTCTTCTTAAGTTATGGTGCAACCCAACACTGCT 1141 1123 CAATGTCACAATAAAAGTGCTATAGGCTCCCACACAGTTAAAAGAAATT 1182 1142 CAATGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACAGTTAAAAGAAGATT 1201	AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATACTCG	AATCAAAAAACATCTCTCCGGAAATGGTGAATTTCAAGCATCCTCAAACACACATGAAACAAAAACATCTCTCTC	AGCATTGCATTGTGCTGCATCTCCATATCCCAAAGAAAGGAAATATGTGAA 	GCTAAGAAAGGAGGAAACATGAATGAAAGACTAAAGAATTCTTGACTCCTCTGCAGGT 14

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3602 TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGAAAACA 3661
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2; TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour; cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of tumour cell. The methods are useful for screening for a bloactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive gent capable of modulating a cell cycle protein tankyrase H or PARP (poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence encodes the tankyrase H isoform 2, TaHo-2, isolated from clone K23 which is described in the disclosure of the invention
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                                                         3662 GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG
                                                                                                                            3722 ATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCATGAAGCAGGAGTGG
                                    3643 GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG
                                                                                                           3703 ATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTGG
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                                                                                                                                                                                                       CCICTACGITITACICCITIGCTGAAAAAAAAA 3816
                                                                                                                                                                                  CCTCTACGTTTTACTCCTTTGCTGAAAAAAAAA 3797
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P-PSDB; ABG73731.
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Query Match 89.4%; Score 3393.4; DB 8; Length 3816; Best Local Similarity 99.9%; Pred. No. 0; 1; Indels 0; Gaps 0; Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 403 AGGTTTTGGGCGGAAAGACGTGATTGATATTGCTTCAGAATGCTCCAAGTCAAGC 462	AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCCAATGCTCGAGATAATTGGAATTATAA AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATATA AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATATA TCCTCTCCTC	602 TCCTCTCCAFGAAGCTGCAATTAAAGGAAAGATTGATFTTGCATTGTGCTGTTACAGCA 661 643 TGGAGCTGAGCCACCATCCGAAATAAAGGAAGGACGACAGCATTGGATTTAGCAGATCC 702	703 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTTTAGAAAGTGCCAG 762 111111111111111111111111111111111111	782 GAGTGGCAATGAAGAAAATGATGGTGCTCTACTCACCATTAAATGTCAACTGCCACGC 841 823 AAGTGGTGGCAGAAAGTCAACTCCATTACATTTGGCAGGATATAACAGAGTAAAGAT 882 842 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGGAGATAAAAAGAATAAAAGAATAAAAGAATAAAAAGAATAAAAAGAAATAAAAAA	tgtacagctgttactgcaacatggagctgatgtccatgctaaagataaaggtgatctggt 	943 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCA 1002 	1003 TGGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTC 1062 	.1063 TAAGAACAGGGTTGAAGTATGTTCTTCTTTAAGTTATGGTGCAGACCCAACACTGCT 1122 	1123 CAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACCACCACCAGTTAAAAGAAAG	1183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG 1242 	MAAAC 13	AGCATTGCATTGTGCTGCTGCATCTCCAAAAAAAAAAAA	GCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT 14

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product= "Human tankyrase homologue isotype
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                                                                            Tankyrase H cell cycle protein; p21; gene therapy;
bioactive agent screening; cancer; cytostatic; gene; human;
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tankyrase homologue isotype 2 (TaHo-2) DNA
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The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (TaHo), comprising an amino acid sequence having 85% or more sequence identify to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (1) diagnosing cancer, which involves determining the activity of (I) fixom a test sample of an individual and comparing the level with a control, (2) treating (M1) an individual with a cell cycle related disorder, which involves administering to the individual an inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (II), comprising a nucleic acid that hybridizes under high stringent conditions to a sequence complementary to the 3797 base pair sequence of ADY97760, or a nucleic acid having 85% or more sequence identity to ADY97760, or a nucleic acid having 85% or comprising (III) comprising (III) operably linked to regulatory sequences recognized (III) comprising (III) or (IIII); (6) producing (I); (7) a polypeptide that comprising (III) binds to (1); and (8) inhibiting (M2) growth of a tumor specifically binds to (1); and (8) inhibiting (M2) growth of a tumor cell, involves contacting the tumor with a bioactive agent capable of
               3703 ATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTGG 3762
                                     cycle; cancer; cytostatic; tankyrase homologue isotype 2; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase homolog, useful for screening its modulator.
                                                                                                                                                                                                                                                                                                                                            Human tankyrase homologue isotype 2 encoding cDNA SEQ ID NO:2.
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25-0CT-2000; 2000US-00696668.
25-APR-2001; 2001US-00843159.
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P-PSDB; ADY97762.
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inhibiting TaHo activity. (I) is useful for screening a bloactive agent capable of modulating (I), or screening for agents capable of interfering with the binding of (I) and P21. (M1) is useful for treating an individual with a cell cycle related disorder. (M2) is useful for inhibiting growth of a tumor cell by a bloactive agent e.g. antisense oligonuclectide. The present sequence encodes the human tankyrase homologue isotype 2.
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                                                                                                                                    Gaps
                                                                                                           Query Match
89.4%; Score 3193.4; DB 14; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; (
                                                                                        Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;
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1482 1542 1362 1441 1561 1602 1662 1681 1722 1741 1782 1801 1842 1902 1962 2022 2082 2202 2221 2262 2281 2401 GCCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT GGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC AACTGTAAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGAGACATTGAAGGGGGGTCA GTCTACACCACTTCATTTTGCAGCTGTGTGTAAACAGAGTGTCCGTGGAGATATCTGCT ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACCTTTGCACAATGC AIGITCTTAIGGACATTAIGAAGITGCAGAACTICTIGITAAACAIGGAGCAGTAGTTAA ATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA TACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA GCTAAGAAAAGGGGGAAACATCAATGAAAAGACTAAAAGAATTCTTGACTCCTCTGCGC CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC **ATTAGGTAATTCAGAGGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGA** AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGCGTCA GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT ACAGCATGGAGCTGATGTGCTAAAAGATAAAAGGAGGCCTTGTACCTTTGCACAATGC TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATGA TACTCCTTTGGATCTTGATAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA AGCTGGTTATAATTTTAGAAGTTGCAGAGTATTTGTTACAACACGGAGCTGATGTGAA GCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT TGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTC TCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGACATTCAACACCTTTACATTAGC 1562 1742 1303 1322 1363 1382 1423 1442 1483 1502 1543 1622 1663 1682 1723 1783 1802 1843 1862 1903 1922 1963 1982 2023 2042 2083 2102 2162 2222 2263 2282 2342 1603 2143 2203 2323 8 6 g & 유 d ઠે g 셤 g 셤 g g 8 ਨੇ 8 ∂ 8 à ઠે ઠે ò 셤 ⋧ ò g ठे 임 8 셤 ઠે 셤 δ g 8 셤

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The present sequence is a version of the human tankyrase II coding sequence. Its protein is thought to be involved in signal transduction in the cell, and to have binding activity for other telomere-associated proteins. It is possible that it plays a role in the regulation of telomere length, thus affecting the replicative ability of the cell. The protein is useful for ribosylating target proteins, for determining tankyrase II binding activity in a sample, and for modulating telomere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding the polypeptide useful for modulating or maintaining telomere length, replicative capacity, apoptosis, chromosome packing or gene expression.
CAGATCTTGTTACATTTGCCACAGCAGCTGCTCTTTTTGCCGGGTAACCTTGGGAAAGTC
                                                   TITCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCAC
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                     TGTAGCAGCTCTAATAAAGTATAATGCATGTGTCAAATGCCACGGACAAATGGCCTTT
                                                                    CACACCTTTGCACGAAGCAGCCCAAAAAGGGACGAACACAGCTTTGTTGTTGTTGCTAGC
                                                                                    CCATGGAGCTGACCCGACTCTTAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC
                                                                                                                                                         CCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC
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SPANK; SAM; sterile alpha motif; PARP; insulin resistance; poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK; ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4; adipocyte; insulin signalling pathway; hyperlipidaemia; glucose intolerance; atheromatous disease; atherosclerosis; obesity; cardiac insufficiency; ocronary insufficiency; stroke; high blood pressure; non-insulin dependent diabetes; hypertension; hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds.
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                                            3661 TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACA
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/product= "Human SPANK"

/transl except= (pos:768. .878,aa:173. .209)

/transl_except= (pos:1230. .137,aa:327. .362)

/transl_except= (pos:1230. .1445,aa:375. .398)

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/transl_except= (pos:2172. .2282,aa:641. .677)
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an ANK domain composed of ankyrin repeats. SPANK is a cytosolic protein which can polytyADP-ribosyl) are itself. SPANK binds insulin-responsive cubich can polytyADP-ribosyl) are itself. SPANK binds insulin-responsive minopeptidase (IRAP) and modulates translocation of GLUT4 in the perinuclear region of adipocytes. It is an effector in the insulin signalling pathway in eukaryotic cells. SPANK is useful for reducing body cass, reducing glucose intolerance or insulin resistance, for preventing cor treating obesity-related diseases or disorders, such as obseity, cardiac insufficiency, coronary insufficiency, stroke, hypertension, atheromatous disease, atherosclerosis, high blood pressure, non-insulin dependent diabetes, hyperlipidaemia, hyperuricemia and Syndrome X and is also useful for preventing or treating muscle-related diseases or disorders, such as muscular dystrophy, muscle atrophy and muscle fatigue. Antibodies immunospecific for SPANK are useful for detecting the presence CS of SPANK polypeptide in a biological sample
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1962 1242 1348 1362 1422 1468 1482 1542 1588 1842 1888 1902 1948 2008 2022 2068 2128 2142 2202 1602 1648 1662 1708 1722 1768 1782 2082 2248 2308 1183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAAAGCTGATGTTACTCG AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACCTTTGCAATGC 1949 ATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAAAAAAATATGA 1243 AATCAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACAGATGAAGC AGCATTGCATTGTGCTGCTGCATCTCCCAAAAGAAAGCAAATATGTGAACTGTT GCTAAGAAAAGGGCGAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT GCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT TAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATCT 1543 ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGGG ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCTTCAGGG CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC ATTAGGTAATTCAGAGGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGA 1723 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGCGTCA GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACCTTTGCACAATGC ATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAAGGAAAATATGA TACTCCTTTGGATCTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA TACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGAGA TCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGACATTCAACACTTTACATTTAGC GGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC 1229 1349 1529 1603 1769 1889 1289 1303 1363 1409 1423 1483 1589 1649 1709 1783 1829 1843 1963 2023 2069 2083 2129 2143 2189 2203 1663 1903 2009 셤 셤 임 g ò a 8 ద 셤 g à g 8 셤 ઠે 셤 ò Š ઠે ò g ઠે 셤 ઠે 셤 ò 셤 ઠે 셤 ò ò ò 셤 à

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The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SNORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere
3389 AAGGCAFGCGFACATAGGFGCATATGGAGCTGGCATTTATTTTGCTGAAAACTCTTC
                                                                CAAAAGCAATCAATATGTATATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAAGA
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                                                               TGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGA
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8883	length, in which TRF1 has a role, is linked to ageing and cancer. sequences are useful in the treatment of cancers and inflammatory disorders
\$ 8°	Sequence 4127 BP; 1245 A; 813 C; 934 G; 1135 T; 0 U; 0 Other;
Oue Ber Mai	<pre>nuery Match</pre>
ò	403 AGGITITIGGGCGGAAAGACGIAGIIGAAIAITIGCIICAGAAIGGIGCAAGIGICCAA
q	208 AGITITGGGCGGAAAGACGTAGITGAATATTTGCTTCAGAATGGTGCAAATGTCCA
ò	463 ACGTGATGATGGGGGCCTTATTCCTCTTCATAATGCATGC
đ	268 Acgreareareseccrraricererraresecrerriresecarecare
දි දි	523 AGTCAATCTCCTTTTGCGACATGCTGCAGACCCCAATGCTGGGATAATTGGAATTAI
à	3 TCCTCTCCAT
අු	388 TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGITTGCATTGTGCTGTTACA
ò	643 TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGA
a	448 TGGAGCCTGAGCCATCCGAATTGGATGGAAGGACAGCATTGGATTTAGCAGA
ờ	703 AICTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGACTCTTAGAAAGTGCC
qа	508 Arcrigicaaagcagrigictracrigiraaaaaaagaagaagrigi
ò	763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCAC
đ	568 GAGTGGCAATGAAGAAAATGATGGCTCTACTCACCATTAAATGTCGACCA
ò	823 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAA
ପ୍ର	628 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAA
δí	883 TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTC
g Q	89
ð	943 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAC
අ	748 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTTGGTCAA
ò	0
셤	808 TGGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGC
ð.	1063 TAAGAACAGGGTTGAAGTATGTTCTCTTTTAAGTTATGGTGGAGACCCAACACTC
qa	868 raagaacagggrigaagrargricriricriraagriarggaggaccaacacr
ò	1123 CAATTGTCACAATAAAAGTGCTATAGACTTCGCTCCCCACACAGTTAAAAGAAAG
q	928 caattgrcacaaraaaagrgctatagactrggcrccacacacagaraaaaaaaa
ò	1183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACT
q	988 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAAGCTGATGTTAC
ò	1243 AATCAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGA
අු	1048 AATCAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACTGA

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463	ACGIGATGGAGGGCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGT 522
523	AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATAC 582
583	TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGCA 642
643	TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC 702
703	ATCTGCCAAAGCAGTGCTTACTGGTGATATAAGAAAGATGAACTTTAGAAAGTGCCAG 762
763 568	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGC 822
823	AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
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1003	TOGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCGGCTTC 1062
. 868	Taagaacagggttgaagtatgttctctttctttaagttatggtgcagacccaacactigct 1122
1123	CAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACCACCAGTTAAAAGAAAG
1183	183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG 1242
1243	AATCAAAAACATCTCTCTGGAAATGGTGAATTTGAAGCATCCTGAAACACATGAAAC 1302
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1482 1287 1542 1347 1602 1407 1662 1467 1722 1527 1782 1587 1842 1647 1902 1707 1962 1767 2022 1827 2082 1887 2142 1947 2202 2007 2262 2067 2322 2127 2382 2187 2442 2247 1422 ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGAGATCCTAACATTATATATCCCTTCAGGG ATTAGGTAATTCAGAGGCAGACAGACAGACTAGTTGCTGGAAGCTGCAAAGGCTGGAGAGATGTCGA 1528 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGGGGTCA 1888 TACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGAGA 1948 TGCAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTAGCCAGAGTGAAGAAGTTGTTTTC TGCCCAAGACAAAGGGGGCTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGA ACAAACCTGCCGCCTACTCCTCAGCTATGGGTGTGATCCTAACATTATATCCTTCAGGG CTTTACTGCTTTACAGATGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC ATTAGGTAATTCAGAGGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGA GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACCTTTGCACAATGC ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTTGCTTTGCACAATGC TCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGACATTCAACACCTTTACATTTAGC **AGCTGGTTATAATATATAAAGTTGCAGAGTATTTGTTACAACACGGAGCTGATGTGAA** TGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGA GCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT GGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC AACTGTAAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGGCGTCA GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGAATATCTGCT TACTCCTTTGGATCTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA TGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTC 1228 1483 1288 1543 1348 1408 1468 1723 1783 1588 1843 1648 1903 1708 1963 1768 1828 2143 2203 2008 2263 2068 2323 2383 1363 1423 1603 1663 2023 2083 9 6 QQ g g ò 셤 QQ 8 g 중 염 d g g 요 6 6 6 g B & ઠે g δ 8 ò à 8 ઠે ò ਨੇ Q ò ద us-10-616-101-1.rng

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                    CACACCTTTGCCACGAAGCAGCCCAAAAAGGGACGAACAACAGCTTTGTGCTTGTTAGTTGCTTTGTTGCTAGC
                                                                             CCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC
                                                                                                                                          AGCAGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTTG
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ö The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telemere-specific binding protein. The regulation of telemere length, in which TRF1 has a role, is linked to ageing and cancer. The equences are useful in the treatment of cancers and inflammatory ሯ New tankyrase2 polypeptides, useful for treating conditions mediated poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders. Gaps Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging; inflammatory disorder; ds. Query Match 89.2%; Score 3387.2; DB 5; Length 4406; Best Local Similarity 99.9%; Pred. No. 0; Matches 3389; Conservative 0; Mismatches 3; Indels 0; Sequence 4406 BP; 1268 A; 910 C; 1054 G; 1174 T; 0 U; 0 Other; Human tankyrase2 clone consensus oligonucleotide SEQ ID NO: Mcelligott DL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tankyrase2 polypeptides, useful for treating conditions mediated by poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-tibosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory
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                                                                                                                                                                                                                                                                                                 Human tankyrase2 TANK2-SHORT coding sequence SEQ ID NO: 134
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0;
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                                                                    Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm;
inflammatory disorder; ds.
                                                                                                                                                                                                                                                                                                                                 New tankyrase2 polypeptides, useful for treating conditions poly(adenosine diphosphate-ribose) polymerase activity e.g. inflammatory and autolmmune disorders.
                                                Human tankyrase2 TANK2-LONG coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                     Mcelligott
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haemostatic, vulnerary, fungicide, antibacterial, virucide, protozoacide, antiarthritic, gene, ss.

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New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neutoimmune, genetic, myeloid or lymphoid, or platelet

or coagulation disorders.

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Ren

Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, F Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M; Wehrman T, Wang J, Wang D, Drmanac RT;

WPI; 2002-759812/82.

P-PSDB; ABP69457

05-MAR-2002; 2002WO-US005095 05-MAR-2001; 2001US-00799451

Homo sapiens. WO200270539-A2.

12-SEP-2002

(HYSE-) HYSEQ INC.

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The invention relates to an isolated polynuclectide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-BZ12166) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynuclectides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellopicative disorders (cancer), neurodegenerative diseases (Parkinson's proliferative disorders (cancer), neurodegenerative diseases (Parkinson's diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 556; 1012pp + Sequence Listing; English.
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0; Mismatches
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Matches 3389, Conservative
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Human, genome mapping, gene therapy, food supplement, virus, fungus, cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease, Alzhelmer's disease; autolmmune disease, multiple sclerosis, diabetes; genetic disorder; wound; burn; infection; arthitis, cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

Human polynucleotide SEQ ID NO 556.

(first entry)

20-JAN-2003

ABZ11674;

ABZ11674 standard; cDNA; 5075

ABZ11674

222 GATGGGGCACAGGGGCTGAAGGAATTGGAATCAATGCTTATGGCACATAGGCACAAACT 2970 GATGGGGCAAGGGGCTGAAGGAATTGGAATCAATGCTTATGGCACATAGGCACAAACT 2981 AATTAAAGGACTCCAAGGACTTATCCAAACTTTAAAGGTTTAAACTT 2982 AATTAAAGGACTCCAGAAGACTTATCCAAAACTTTAAACTTT 2983 AATTAAAGGACTCCAGAAGACTTATCAAAACTTTCAAAGATTTCAA 2990 GAACCTCTGGTAGTGAACAATTCTTAATAATCTGTCTCTCATGATAAAAAGTTTCAA 2990 GAACCTCTGGAAGAACATTCTTAATAATCTGTCTCTCATGATAAAAAGTTTCAAG 2910 GAACCTCTGGAAGAACATTCTTAATAATCTGTCTCCTCATGATAAAAAGTTTCAAG 2910 GAACCTCTGGAAGAACATTCTTAATAATCTGTCTCTCATGATAAAAACTTTCAAG 2911 GAACCTCTGGAAGAACATACTCTAAAATTCTCAAAGTTTCAAGAAACTTTC 2911 GAACCTCTGGAAGAACATACTCAAAATTCTCAAAGTTTCAAAAACTTTC 2911 GAAACATCAACAAAAATTCTCAAAATTCTCAAAAGTTTCAAAAAACTATG 2911 GAAACATCAACAAAAATTCTCAAAATTCTCAAAAGTTTCAAAAACAATG 2911 GAAACATCAACAAAAATTCTCAAAATTCTCAAAAGTTTTTAAAAAAACAATG 2911 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
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AU140145 AU140145
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genome Conter (GSC), Kanagawa, 230-0045, Japan (E-mail:genome-reseascriken:jp, Nokohama, NELSHUR: 181-45-503-9212.
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Mackrgglypthaacsyghyratellkdgavhadlwgrpthlearblakvrycsl
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TPLHPAAGYNRVSVVEYLLHGADVHAKDKGGLVPLHNACSYGHYEVAELLVRHGASV
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Inote="unnamed protein product; putative
tankyrase, TRF1-interacting ankyrin-related ADP-ribose
polymerase (MGD|MGI:1341087 GB|AA415426, evidence: BLASTN,
99%, match=439)"
                                                                                                                       Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1663 (2005)

Research to 3417)
                                                                            The FANTOM Consortium, the RIKEN Genome Exploration Research Group
                                                                                                                                                                                                                        RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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RGDAALLDAAKGGLARVQULCTPRNIVCRDTOGRUSTSTPLHLAAGYNNLEVAEYLLEH
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42.4%; Score 1609.8; DB 6; Length 3417; 72.4%; Pred. No. 0; i.ive 0; Mismatches 782; Indels 27; Query Match
Best Local Similarity 72.4
Matches 2126; Conservative

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LION N 80

AK149368 2226 bp mRNA linear HTC 21-SEP-2005 Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730001F05 product:Tankyrase 2 (EC

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi, Y., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Osaokori, T., Bono, H., Kasukawa, T., Yamanaka, I., Kadota, K., Isawa, T., Kasukawa, T., Zasito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchl, P., Lewis, S., Matsuo, Y., Nikaido, I., Fuzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Schonbach, C., Seya, T., Shibata, Y., Saroch, K., Schonbach, C., Seya, T., Shibata, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
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2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1- interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein) homolog [Homo sapiens], full insert
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Nature 420 (6915), 563-573 (2002)
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Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H.,
Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T.,
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Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A.,
Wahlestedt, C.
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Antisense transcription in the mammalian transcriptome
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                                                                                                                                                                                                 Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, VRL:http://genome-gsc.riken.jp, 7-181-45-503-9216)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1- interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein) homolog (Homo sapiens) (UniProt | Q912K2, evidence: FASTY, 96.8% ID, putative
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/db_xref="RANTOM DB:C730001F05"
/db_xref="taxon:10090"
/clone="C730001F05"
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Pred. No. 0;
0; Mismatches
      309 (5740), 1564-1566 (2005)
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/db_xref="GI:74143549"
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llarity 89.7%;
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Muramacul, m. anayashirzakii.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Physical and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-resegnec.riken.jp, VRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                              TPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFG
HAVNALLQHGAHPNARDNINYTPLHAAAIKGKIDVCIVLACHGGAEPFTRNTDGRTA
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OFTPLHEAASKNRIBVCSLLLSYGADPTLLNCHKSAIDLAPTAQLKERLSYERGHS
LLQAAREADVTRIKKGLSLENWYFGHPQTHETALHCAASPYPKKKGICELLKKGAN
TNEKTKGFLTPLHVASENAHNDVVEVVVKHBAKVNALDSLGGTSLHRAAHCGHLQTCR
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| db_xref="taxon:10090"
| clone="p930018021"
| tissue_type="cerebellum"
| clone_lb="RIKEN full-length enriched mouse cDNA library"
| dev_stage="10 days neonate"
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                                                  The FANTOM Consortium, the RIKEN Genome Exploration Research Group Mahase I and II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                            RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
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/mol_type="mRNA"
/strain="C57BL/6J"
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/proteIn_id="BAC32960.2"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
Nature 409, 685-690 (2001)
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Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone: B930018021 product: TANKTRASE-RELATED PROTEIN (FRAGMENT) homolog (Homo sapiens), full insert sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC, CAP trapper.
Mus musculus (house mouse)
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL PUBMED

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AKO80913
3194 bp mRNA linear HTC 02-SEP-2005
MUS musculus 4 days neonate male adipose CDNA, RIKSN full-length
enriched library, clone: B430206N15 product: TRF1-INTERACTING
ANKYRIN-RELATED ADP-RIBOSE POLYMERASE homolog [Homo sapiens], full
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                     TAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATCT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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KKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLOHGADVHAKDKGGLVPLHNA
CSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAA"
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36.1%; Score 1369.8;
Best Local Similarity 90.8%; Pred. No. 0;
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/note="TRF1-INTERACTING ANKYRIN-RELATED ADP-RIBOSE POLYMERASE homolog [Homo sapiens] (SPTR|095271, evidence: PASTY, 95.9%ID, 80%length, match=3167)
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                                       Konno, H., Akiyama, J., Nishi, K., Kifeunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, R., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Yonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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/clone_llb="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phase I and II Team. Manayers of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
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/strain="C57BL/64"
/db_xref="FANTOM_DB:B430206N15"
/db_xref="taxon:10090"
/clone="B430206N15"
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           Itoh, M., Aizawa, K.,
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Mielsen, R., Bustamante, C., Tamenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (OS-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Fockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,

White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

Chimpanzees

(er) PLOS Biol. 3 (6), E170 (2005)
                                          TTACTCCCCTTCACGAAGCTGCCCAGAAAGAAGGACGCAGTTATGTGCCCTGCTCCTAG
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    /organism="Homo sapiens"
    /mol_type="genomic DNA"

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                                  | TGCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACG
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                                                                                        Gaps
                                                                    Score 1221.6; DB 14; Length 3612;
Pred. No. 0;
0; Mismatches 1020; Indels 69;
/db_xref="taxon:9606"
/chromosome="8"
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/gene="TNKS"
/locue_tag="HC3703"
                                                                    Query Match 32.2%;
Best Local Similarity 63.2%;
Matches 1872; Conservative
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Hominidae; Pan.
1 (bases 1 to 3107)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.
Hubiss, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                          Mieleen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Mieleen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xreff"taxon:9598"
                                                                                                                                                                               PLoS Biol. 3 (6), E170 (2005)
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              troglodytes (chimpanzee)
                               Pan troglodytes
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               Pan
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49.2%; Pred. No. 2.8e-226;
tive 0; Mismatches 1255; Indels
<li....>3107
/gene="TNKS"
/locus_tag="HC3703"
                                                                                                    Query Match
Best Local Similarity 49.2'
Matches 1275; Conservative
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DQ034115

Ban troglodytes TNKS gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DQ034115.1 GI:66885324

DEFINITION ACCESSION VERSION

RESULT 6 DQ034115 LOCUS

Db 3060 TGTCACAGCAGCAGCAGGAGAGAGAGAGAGAGAGAGAGAG	DD RES CR9	TATANTOCATO CONTROLLANDOCATOR CONTROLLO CONTRO	6 6 6
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888 bp mRNA linear EST 24-JUN-2005 no.9017 Homo sapiens cDNA clone RZPDp9017K2313 5',

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CR987822 RZPD no.9016 Homo sapiens cDNA clone RZPDp901611435 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 926)
Hell.O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D. and Korn, B.
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http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
                                                                                                                                                               421 AAACTAATTAAAGGAGTCGAGAGAGACTTATCTCCGGACAACAACAAGGTCTTAACCCATATTA
                                                                                                                                                                                                                                                                                               3038 ACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAGATCTGTCTCCTGATGATAAAGAG
                                                                                                                                                                                                                                                                                                                  GCAGGTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAA
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
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KZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
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Unpublished (2005)
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPD; RZPD; RZPD LIB NO.9017
RZPD; RZPD; RZPD; Human T-Lymphocytes) RZPD LIB NO.9017
http://www.rzpd.de/cgi.bin/products/set.cgi?libNo=9017 Contact:
Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9017K2313
contact RZPD (product-support@rzpd.de) for further information.
Primer name: qe3 4, primer sequence: CGGATAACAATTCACACAG.
Location/Qualifiers
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                           Hominidae; Homo.
1 (bases 1 to 888)
Hell,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RZPD no.9017"
/note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="T-Lymphocytes"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="RZPDp9017K2313"
                      CR983155
CR983155.1 GI:68221489
                                                                                Homo sapiens (human)
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885; Conserva
                                                                                                    Homo sapiens
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Hominidae, Homo.

I (bases I to 838)

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Kimura,K., Wakamatsu,A., Sekine,M., Tsuriteni,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Wurakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Exax: 81-438-52-3986
Exax: 81-438-52-3986
Exail: fll-cdnagarifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
600 ACCCAAGGCAGACATTCAACACTTTACATTTAGCAGCTGGTTATAATATTAGAAGTT
                                                                                                                                                                                                                               2468 AAGGGACGAACACAGCTTTGTGCTTGCTAGCCCATGGAGCTGACCCGACTCTTAAA
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                                                              660 GCAGAGTATTTGTTACAACACGGAGCTGATGTGAATGCCCAAGACAAAGGAGGACTTATT
                                                                                                                          2348 CCTTTACATAATGCAGCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGTAT
                                                                                                                                             720 CCTTTACATAATGCAGCATCTTACGGGCATGTAGAATGTANCAGCTCTACTAATAAAGTAT
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FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 838;
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                                                                                                                                                                                                                                                                                                                                                                          2528 AATCAGGAAGGACAAACACCTTTAGATTTA 2557
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                                          This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016I1435
contact RZPD (product-support@rzpd.de) for further information.
Primer name: qe3 4, Primer sequence: CGGATAACAATTCACACAG.
Location/Qualifiers
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      Fax: +49 30 32639 111
www.rzpd.de
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/tissue_type="Ascending colon"
/dev stage="6 months old fetus"
/dab_host="E. coli DH10B T1 Phage Resistant"
/clone lib="GC BGC-17"
/note="Organ: Ascending colon; Vector: pExpress 1; Site_1:
Blunt (5' end of cDNA); Site_2: NotI (3' end of cDNA)"
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Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaiff, R., Baland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R., Stott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A. Bovine Genome Sequencing Program: Full-length cDNA Sequencing Unpublished (2005)

Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
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                                                                                                                                                                       Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
Canada, V5Z 486
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-73561
Email: robertk@bcgsc.ca
Plate: LB0173 row: I column: 4
High quality sequence stop: 898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
/clone="IMAGE:8121774"
                                                                                                                                                                                                                                                                                                                                                                                   organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="L1 Hereford"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bos
1 (bases 1 to 898)
Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,
                                                                                                                                                                                                                                                                              CAAGTGGAACAGAGGCTCCCAGTTTGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTA
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 848)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1528 ATATIGIGGICATCTACAAACCIGCCGCCTACICCTGAGCTATGGGTGTGATCCTAACAT
                                                                                                                                                                                                                                                                                                                                                                   1228 AGCTGATGTTACTCGAATCAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCC
                                                                                                                                                                            714 AATATGTGAACTGTTGCTAAGAAAAGGAGCCAACATCAATGAAAAGACTAAAGAATTCTT
                                                                                                                                                                                                                       1408 GACTCCTCTGCACGTGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAA
                                                                                                                                                                                                                                        1468 ACATGAAGCAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTTCTTCTACACAGAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                              1588 TATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 ACCTITGCACAATGCATGTTCTTATGGACATTATGAAGTTGCAGAGCTTCTTGTTAAGCA
                                                              834 AGCTGATGTTACACGAATCAAAAACATCTCTCTCGGAAATGGTGAACTTTAAGCATCC
                                                                                            1348 AATATGTGAACTGTTGCTAAGAAAGGGGCAAACATCAATGAAAAGACTAAAGAATTCTT
                                                                                                                                                                                                                                                                                                          594 ACATGAAGGAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTTCTTTGCACAGGCTGC
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 Indels
   42;
   0; Mismatches
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   Matches 792; Conservative
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Bos taurus

Bos taurus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

B 1 (bases I to 834)

S Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Caass, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,

Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,

Chitko-Oncown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,

Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle
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                                                                                                                                                                                                                           780
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USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
De Dox 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified w
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/organism="Bos taurus"
/mol_type="mRNA"
/db kype="mRNA"
/tissue_type="pooled"
/tissue_type="pooled"
/tlone_lib="WARC 4B0"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
                                                                ATGITATITACAGAGGAGAACAGGCITATCCIGAGTATITAAITACITACCAGATIATGA
                                                                                                                                                                                                          CTGGATGTCCAGTACATAAAGACAGATCTTGTTACATCTGCCACAGGAGCTGCTCTTGT
                                                                                                                                                                                                                                                                          CTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTT
                                                                                                                                                                                                                                                                                                                     Score 766.8; DB 5; Length 834;
Pred. No. 5.8e-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                  CK847047 834 bp mRNA linear
969630 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.
CK847047
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Plate: 98 row: 1 column: 7
Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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Tel: 81-438-52-3975
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Matches 763;
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                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLK8064 row: G column: 17
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
| /organism="Bos taurus" / /organism="Bos taurus" / /mol_type="mRNA" |
//db_xref="taxon:9913"
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
PT 11: 402 762 4366
Pax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                    /tissue type="pooled"
/lab host="PHIOB"
/clone lib="MARC 780V"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tIssues
including ovary, hindbrain, uterus, and day-30 whole
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Best Local Similarity 91.5%;
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I (Dases I to 819)

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Kimura,R., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Eujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1584
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                                                                                                                                                                                                                                                                                         794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: flj-cdna@nifty.com
HRT human cDNA project; 5. - & 3'.end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department o
Virology, Institute of Medical Science, University of Tokyo, and
675 cccrracarrragcaccrecrrararararrragacrracceaararrcrccracacar
                                                                                                                                                                                                                                 2309 GGAGCTGATGTGAATGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCAGCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1525 TGCATATTGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAA
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                                                                                                     2249 CCTTTACATTTAGCAGCTGGTTATAATATTTAGAAGTTGCAGAGTATTTGTTACAACAC
                                                                                                                                                                                                                                                                                      735 GGAGCTGATGTGAATGCTCAGGACAAAGGAGGACTTATCCCTTTACACAATGCAGCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA733094 B19 bp mRNA linear EST 09-NO DA733094 NT2RP2 Homo sapiens CDNA clone NT2RP2002155 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                     846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2R2"
/clone_lib="NT2R2"
/ntc="Vector: pME18SFL3; mRNA from NT2 neuronal
cells after 2-weeks retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                           2369 TACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGTATAATGCATGTGTCAA
                                                                                                                                                                                                                                                                                                                                                                                        2
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Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 819;
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ilarity 93.0%; Pred. No. 3.5e-173;
Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .819
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="NT2RP2002155"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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/ mol type="mina" "maculus" | // mol type="mina" | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2936 GAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTC 2995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGGGTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTAC 3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGGTGGAATCTTCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2876 ATGGATATATTTGAGAGAGCAGATCACTTTGGATGTATTAGTTGAGATGGGGCCACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATGGATATATTTGAGAGAGAGAGATTACCTTAGATGTCCTAGTTGAAATGGGCCACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2996 GAGAGACTTATCTCCGGACAACAAGGTCTTAACCCATATTTAACTTTGAACACCTCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAAAGGCTGATCTCTGGACAAGGTCTTAATCCATATTTAACTCTAAACAACTCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AGATACAACATTCTCAAGATTCAGAAGGTTTGTAACAAGAAATTGTGGGAAAGATAAACA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can l

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov column: 01

Plate: NDAW0316 row: o column: 01

High quality sequence stop: 779.
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18.1%; Score 687.8; DB 4;
Best Local Similarity 88.5%; Pred. No. 8.1e-172;
Matches 768; Conservative 0; Mismatches 98;
                                                                                                                                                                                                                                              1. .955
/organism="Mus musculus"
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Chordata; Craniata; Glires;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 955)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTACCTTTGCACAATGCATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAA
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                                                                                                                                            AAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAG
                                                                                                                                                                                                                                                                                                                                  AGACATTGAAGGGCGTCAGTCTACACCTCATTTTGCAGCTGGGTATAACAGAGTGTC
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        CATTATATCCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACT
                                                                                                                AAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTGGTGGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCT
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AGENCOURT 11385409 NIH MGC 164 Mus musculus cDNA clone
IMAGE:30244272 5', mRNĀ sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACAACACGGAGCTGATGTGAATGCCCAAGACAAAGGAGG 2340
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1 (bases 1 to 675)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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21C Frontier Korean BST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
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523 3 US-09-196-387-12 Sequence 523 3 US-09-841-835-12 Sequence 14770 3 US-09-220-132-30 Sequence	2.6 14/70 3 03-03-949-016-110/ sequence 2.4 5235 2 US-09-031-485-35 Sequence	4 5235 2 US-09-031-485-36 Sequence	2.4 5235 2 US-08-847-429A-35 Sequence 35,	2.4 5235 3 US-09-065-474-35 Sequence	2.4 5235 3 US-U9-U55-4/4-36 Sequence 36,	2.4 5235 3 US-09-557-034-36 Sequence	2.4 5503 2 US-09-031-485-32 Sequence 32,	2.4 5503 2 US-09-031-485-34 Sequence 34,	2.4 5503 2 US-U8-84/-429A-32 Sequence	2.4 5503 3 US-09-065-474-32 Sequence 32.	2.4 5503 3 US-09-065-474-34 Sequence 34,	2.4 5503 3 US-09-557-034-32 Sequence 32,	33 . 2.4 5503 3 US-09-557-034-34 Sequence 34,	2.4 . 8560 3 US-09-949-016-1788 Sequence 1788	ALIGNMENTS	1	-899	Sequence 1, Application US/09696668 Datent No. 6617102	GENERAL INFORMATION:	н	APPLICANT: Chan, Eva		APPLICANT: Huang, Betty	THE REPORT OF THE POST OF THE	COMPOSITIONS INVOLVED IN THE CELL	CURRENT APPLICATION NUMBER: US/09/696,668	CURRENT FILING DATE: 2002-07-23	PRIOR APPLICATION NUMBER: US 09/427,154	PRIOR FILING DATE: 1999-10-25		SOFTWARE: Patentin version 3.1	ENGLIN O. 1	PENGIN: ANA	11FE: DNA ORGANISM: Homo sapiens	-09-696-668-1	100.0%; Score 3797	Best Local Similarity 100.0%; Pred. No. 0; Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	0.3	
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CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1321 TGCATCTCCATATCCCAAAAGCAAATATGTGTAACTTGTTGTTAAGAAAAAGGAGCAAA 138

දු පු	2461 AGCCCAAAAGGGACGACACAGCTTTGTGCTTTGTTGCTAGCCCATGGAGCTGACCCGAC 2520	3541 AATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAA
ት 8	2521 TCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTTCAGCGGATGATGTCAGCGC 2580 	
& g	581 TCTTCTGACAGCGATGCCCCCATCTGCTCTGCCCTCTTGTTACAGCCTCAAGTGCT 264	3661 AATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGGATAATAGTTATTTAAG
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& g	2701 ATCAAGCCTTTCTGCAGCCAGCAGTCTTGACAACTTATCTGGGAGTTTTTCAGAACTGTC 2760 	Oy 3781 TTGCTGAAAAAAAAA 3797 DD 3781 TTGCTGAAAAAAAA 3797
දු අ	2761 THCAGTAGTHAGTHCAAGHGGAACAGAGGGGCTHCCAGTHTGGAGAAAAAGAGGGGGTHCC 2820	RESULT 2 US-09-843-159B-1 ; Sequence 1, Application US/09843159B
9 9	2821 AGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATGGA 2880 	; FACETE NO. 28876.7 ; GENERAL INFORMATION: ; APPLICANT: Luo, Yin ; APPLICANT: Chan, Evan
g &	2881 TATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTGAGATGGGGCACAAGGAGCT 2940 	APPLICANT: Au, Arang ; APPLICANT: Huang, Betry ; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c ; FILE REFERENCE: A-66292-2-2/RMS/DHR. ; FILE REFERENCE: A-66292-2-2/RMS/DHR.
, 9 9	2941 GAAGGAGATTGGAATCATGCTTATGGACATAGGGAAAATAATTAAAGGAGTCGAGAG 3000 	; CURRENT FILING DATE: 2001-425; PRIOR FILING DATE: 2000-425; PRIOR APPLICATION NUMBER: US 09/696,668; PRIOR FILING DATE: 2000-10-25; PRIOR FILING DATE: 2000-10-25
که م	3001 ACTIAICTCCGGACAACAAGGTCTIAACCCATAITTAACTITGAACACCTCTGGTAGTGG 3060 	; PRIOR AFFILIATION NUMBER: US 09/42/,154 ; PRIOR FILING DATE: 1999-10-25 ; NUMBER OF SEQ ID NOS: 17 ; SOFTWARE: Patentin version 3.1
yo d	3061 AACAATTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTCAGTCTGTGGAGGAAGGA	; SEN TH. 3797 ; TYPE: DNA ; TYPE: DNA ; ORGANISM: Homo sapiens
දු දු	3121 GCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGGTGGATCTTCAACAGATA 3180 	Query Match Query Match Best Local Similarity 100.0%; Score 3797; DB 3; Length 3797; Best Local Similarity 100.0%; Pred. 00. 0; Notation 2707: Contraction of Mismatches 0. Indels 0. Gang 0.
b o	3181 CAATATICTCAAGATICAGAAGGTTIGTAACAAGAAACTATGGGAAAGATACACCGG 3240 	CONSELVACIONE 0; MISHBACCINES 0; INGELS 0; ORDS OF THIRD ARGARD CONTINUES
& 4	3241 GAGAAAAGAAGTITCTGAAGAAAACCACAACCATGCCAATGAACGAATGCTATTTCATGG 3300 	61 AGACAAATATTAGCTGTGAGCAGATCTTTTTTTTTTGCTTGC
& g	3301 GTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGG 3360 	DD 61 AGACAMAIATIAGCIGIGAGCAGAICITITITIGIIGCIICIIGIAAICCCCCAGIIIAG 120 Qy 121 CAGAAACATICTGTGAGATAGATGGGGAAAGGAATTCTAGCAAGAGTTTTGTCACTGTA 180 13. CAGAAACATTCTGTGAGATAGATAGATGTGGGAAAGGAATTCTAGCAAGGATTTTGTCATA 180
& a	3361 IGGTATGTTTGGAGCTGGCATTTATTTTGCTGAAAACTCTTCCAAAAGCAATCAAT	121 CACAMACATICIGIGAGA INGALIGICAGAAN CATATICIAGCAAGA GATTIGICACIGIA 181 TCATAAGGTTGTGATTTACATTTAAGTTTTATACTTTGAACATCTGAAAATGTATACA
<u>ک</u> ۾	3421 ATATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAGACAGAATCTTGTTACATTTG 3480 	181 TCATAAGGTIGTGAATTTACATATTTAAGTTTTATACTTTGAACATCTGAACATGTATACA 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAACATTTGAACTTTGAGCTTTCAGTC
& g	3481 CCACAGGCAGCTGCTTTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGC 3540 	Db 241 TACTAMATATGCAGAACTCTATTGTAGAGACATTTGAACTTTGAACTTTCAGTC 500 Qy 301 ACTTATTTGTATTCTTTGAGGTTAGCAGTACCACCCAAGGCACTGCTTAGGT 360 Db 301 ACTTATTTGTATTCTTTGAGGTTAGCAGTACCACCCCAAGGCACTGCTTAGGT 360
È	3541 AATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAA 3600	

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2521 TCTTAMAMATCAGGAAGACAACACCTTTAGATTTAGTTTCAGCGGATGATGTCAGCGC 2580 2581 TCTTCTGACAGCACATCCTCCTCTCTTTTTTTTTACAAGCCTCAAGTGCT 2640 2581 TCTTCTGACAGCAGCATCCTCCTTCTCTTTTTTTACAAGCCTCAAGTGCT 2640 2581 TCTTCTGACAGCAGCCATCCTCTTCTCTCTTTTTTTTTT	868686	3661 AATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGGATAAATAGTTATTTTAAG 3720
TTCAGTAGTTAGTTCAAGTGGAACAGAGGGTTCCAGTTTGGAGAAAAAGGAGGTTCC 2820 TTCAGTAGTTAGTTCAAGTGGAACACAGAGGAGGTTCC 2820 TTCAGTAGTTAGTTCAAGTGGAACACTCCAGTTTGGAGAAAAAAAA	RESULT US-09-6 1 Second 1 GENEI 2 APPI 1 APPI 1 TITI 1 PRICE 1	RESULT 3 US-09-696-668-2 Sequence 2. Application US/0969668 Factor No. 6617102 GENERAL INFORMATION: APPLICANT: Luo, Ying APPLICANT: Luo, Ying APPLICANT: Au, Xiang APPLICANT: W. Xiang APPLICANT: W. Xiang APPLICANT: Huangy Betty APPLICANT: Huangy APPLICANT: Bungy APPLICATION NUMBER: US/09/696,668 FURREW FILING DATE: 1999-10-25 FRIOR FILING DATE: 1999-10-25 FRIOR FILING FURREW: PATENT: Bungy FRIOR FILING FURREW: Bungy FRIOR FILING FURREW: Bungy FRIOR FILING FURREW: Bungy FRIOR FURREW: Bungy FRIOR FILING FURREW: FURREW: Bungy FRIOR FURREW: Bungy FRIOR FURREW: FURREW: Bungy FRIOR FURREW: FUR
3121 GCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCGTGGAGTGGAATCTTCAACAGATA 3180 	Que: Best Matc	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 3394; Conservative 0; Mismatches .1; Indels 0; Gaps 0;
3181 CAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTATGGGAAAGATACACTCACCG 3240 	& 9	403 AGGITTIGGGCGGAAAGACGIAGITGAATAITTGCTICAGAAIGGIGCAAGIGICCAAGG 462
3241 GAGAARAGAGTTTCTGAAGAARCCACACCATGCCAATGAACGAATGCTATTCATGG 3300 	& g	463 ACGTGATGATGGGGGCCTTATTCCTCTTCATAATGCATGC
3301 GTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGG 3360 	රු අ	523 AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATAC 582
3361 TGGTATGTTTGGAGCTGGCATTTATTTTGCTGAAACTCTTCCAAAGCAATCAAT	& 8	583 TCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGCA 642
3421 ATATGGAATTGGAAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTAGATTTG 3480 	%	643 TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC 702
3481 CCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGGGG 3540 	රු සි	703 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG 762
3541 AAIGAAAAIGGCACAITCTCCCCGGTCAICACTCAGTCACTGGTAGGCCCAGTGAAA 3600 	λ Q	763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACCACTTAAATGTCAACTGCCACGC 822
3601 TGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAACAGGCTTATCCTGAGTATTT 3660 	λo qa	823 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGGAGATATAACAGAGTAAAGGTT 882

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TYPE: DNA ORGANISM: Homo sapiens ORGANISM: Homo sapiens 1.09 843-159B-2 08483-159B-2 08483-159B-2 08484; Score 3393.4; DB 3; Length 3816; Best Local Similarity 99.9%; Pred. No. 0; Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 403 AGGTTTTGGGCGGAAAGACGTAGTTGAATTTGCTTCAGAATGGTCAAGGGAGAAGTGTCCAAGG 462 422 AGGTTTTGGGGGAAAGACGTAGTTGAATATTGCTTCAAATGGCAAATGTCCAAGG 481 463 ACGTGATGATGAGGGGCCTTATTCCTCTTCATAATGCATGC	542 583 602 643 662 703	722 AICIGCCAAAGCAGIGCIIACIGGIGAAIAIAAGAAAGAIGAACICIIAAAAGAIGCCAGG 763 GAGIGGCAAIGAAAAAAATGATGGCTCTACTCACCACCATTAAATGTCAACTGCCACGG 782 AAGIGATGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	902 943 962 1003	1063 TAAGAACAGGGTTGAAGTATGTTCTCTTTAAGTTATGGTGCAGACCCAACACTGCT 1122
S & S & S & S & S	4 6 6 6 6 6	8 6 8 6 8 6	4 6 4 6 4	Methods Oy
	3343 AAGCCATGCTACATAGGGGTATTTTGGACTTGCATTTTTTTT	Oy 3523 TTTCCTGCAGTTCAGTGCAATGAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCCC 3582	3702 ATANATACTUTATATAACTAATTCCACTGAACCTAAAATCATCAAGAGGGGGGGG	RESULT 4 US-09-843-159B-2 Sequence 2, Application US/09843159B Patent No. 6887675 Patent No. 6887675 GENERAL INFORMATION: APPLICANT: Chan, Evan APPLICANT: Chan, Evan APPLICANT: Chan, Evan APPLICANT: Chang, Betty APPLICANT: Chang, Betty TILE OF INVENTION: Tang APPLICANT: Huang, Betty TILE OF INVENTION OF TANGYDHR CURRENT APPLICATION NUMBER: US/09/843,159B CURRENT FILING DATE: 2000-10-25 PRIOR PILING DATE: 2000-10-25 PRIOR FILING DATE: 1999-10-25 PRIOR FILING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PatentIn version 3.1 SEQ ID NO 2

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781 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG 840
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                            GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGC
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                                                                                                                            ATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCATCAAGCAGCAGTGG 3762
                                                                                                                                            3722 ATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCATCAAGCAGCAGGGG 3781
             TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGAGAACA 3642
                               3602 TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACA 3661
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                                                                                                                                                                                                                                                                              Sequence 5. Application US/09972115A
Sequence 5. Application US/09972115A
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gereg, Morin B.
APPLICANT: Watler, Funk D.
APPLICANT: Wieczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase;
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR PILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                   Query Match 89.2%; Score 3388.8; Best Local Similarity 99.9%; Pred. No. 0; Matches 3390; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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	RESULT 6 US-09-799-451-556 ; Sequence 556, Application US/09799451 ; Patent No. 678369 ; GENERAL INFORMATION: ; APPLICANT: Tang, Y. Tom ; APPLICANT: Goodrich, Ryle ; APPLICANT: Ren, Vinod ; APPLICANT: Shou, Yinod ; APPLICANT: And, Yinod ; APPLICANT: Zhang, Jie ; APPLICANT: Zhang, Jie ; APPLICANT: Xue, Aidong J.
1993 ACACCATGGACCGATGCTANAGTANAGAGGACCCTTGACCTTTCCCCANTCC 1990 1991 ACACCATGGACCTGATCCTANAGATANAGAGGACCCTTGACCTTTCCCCANTCC 1990 1991 ACACCATGGACCTGATCCTANAGATANAGATCCCTTTTCCCCANTCC 1990 1991 ACACCTTTCCTACTATATACACTTCCACATACTTCACACACTTCTT	2743 GAGITITICAGAACIGITCITCAGIAGITAGITCAAGIGGAACAGAGGGIGCITCCAGITI 2802 [

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                                                                                                                                                                                                                                                                                                                                                        Length 5075;
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APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Yanazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Duntui
APPLICANT: Wang, Duntui
APPLICANT: Wang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Branac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT PILING DATE: 2001-03-05
CURRENT PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_F_genes Version 2.0
LENGTH: 5075
TURNED: NANA
                                                                                                                                                                                                                                                                                                                                                       DB 3;
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89.2%; Score 3387.2;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (253)..(3750)
US-09-799-451-556
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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1130 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTAACTCG 1290 AATCAAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACATGAAAC 1590 ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGGG CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGGTATCTC 1710 ATTAGGTAATTCAGAGGCAGACAGACAATTGCTGGAAGGCTGCAAAGGCTGGAAGTTGCGA 2130 TACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGAGA CAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACCACAGTTAAAAGAATT AATCAAAAAACATCTCTCTCGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAAC 1543 ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGGG 1650 CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC 1830 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGCT 1903 ATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA 1950 ATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA 1963 TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATGA TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATTAGA TACTCCTTTGGATCTTGTTAAAGATGAGAGATACAGATATTCAAGATCTGCTTAGGGGAGA 1063 TAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAGTTATGGTGCAGACCCAACACTGCT 1110 TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAGTTATGGTGCAGACCCAACACTGCT **ATTAGGTAATTCAGAGGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGA** 1723 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAAACTGCAGAGACATTGAAGGGCGTCA GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTATATCTGCT ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACCTTTGCACAATGC

1603 CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTC				2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTTGTTTAGCCAGAGTGAAGATTGTCTTC 2202 2158 TGCAGCTTTGCTAGTTGTTGCTGTTGTTTTTTTTTTTTT	2263 AGCTGGTTATAATATTAGAAGTTGCAGAGTATTTGTTACAACACGGAGCTGATGTGAA 2322	0 0 0	2443 CACACCTTTGCAACAACAGCAACAAACAACAACAAACAACATTGTTGCTAGC 2502 2458 CACACCTTTGCAACAACAACAACAACAACAACAACAACAACAACAACAA	26	2623 TTACAAGCCTCAAGTGCTCAATGGTGTGAGAAGCCCAGGAGCCACTGCAGATGCTCTCC 2682 [
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AGTCAATCTCTTTTGCGACATGCTGCACACCCCAATGCTCGAGATAATTGGAATTATAC 58	703 718 763 778	y 823 AAGTGATGGCAGAAGTCAACTCCATTACATTTGGCAGGATATAACAGAGTAAAGAT 822 b 1	943 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAACTAACT	TAAGAACAGGGTTGAAGTATGTTCTTTTAAGTTATGGTGCAGACCCAACACTGCT TAAGAACAGGGTTGAAGTATGTTCTCTTTTAAGTTATGGTGCAGACCCAACACTGCT TAAGAACAGGGTTGAAGTATGTTCTCTTTTAAGTTATGGTGCAGACCCAACACTGCT CAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACAGTTAAAAGAAAG	CAATIGICACAAIAAAAGIGCIAIAGACTIGGCICCCCACCCACCAGTIAAAAGAAAGATTAAAGAATTAAAGACCACTGCTGCTGCAAGCAGAAGATGAATTTAAAGGCCACTGCTGCTGCCAGCAGCAGAAGAAGAAGATGAATTTAAAGGCCACTGGTTGCTGCAAGCTGCAGCAGAAGATTTAAAGGCCACTGGTTGCTGCAAGCTGCAGCAGAAGCTGATGATTAAAAGCCCACTGGTTGCTGCAAGCTGCAGAAGCTGCAGAAGCTGCTCC	1243 AATCAAAAACAICTCTCTGGAAAIGGTGAATTTCAACGACCACCATGAAC 1302	1363 GCTAAGAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT	1438 GCCAICTGAGAAGCTCATAATGATGATGATGAGTGAGTGAAACATGAGCAAAGGT 1497 1483 TAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATCT 1542 1498 TAATGCTCTGGATAATCTTGGTCAGATTCTCTACACAGAGCTGCATATGTGGTCATCTTGTTGTGTGTG	ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGGG 16

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Sequence 1, Application US/09427154
; Sequence 1, Application US/09427154
; Patent No. 6589725
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Luo, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: METHODS OF USE
; FILLE REPERENCE: A-68292-DUB/RMS/DAV
; TITLE OF INVENTION: METHODS OF USE
; FILLE REPERENCE: A-68292-DUB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/427,154
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 1.
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                                                                        CCTCTACGTTTTACTCCTTTGCTGAAAAAAA 3611
                                                         CCTCTACGTTTTACTCCTTTGCTGAAAAAA 3794
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Berthelsen, Jens
APPLICANT: Berthelsen, Jens
APPLICANT: Toma, Salvatore
APPLICANT: Tacona, Antonella
TITLE OF INVENTION: Tankyrase Homolog Protei
TITLE OF INVENTION: Tankyrase Homolog Protei
TITLE OF INVENTION: Same
FILE REFERENCE: PHRM 0043
CURRENT APPLICATION NUMBER: US/09/350,982C
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 3291.8;
99.7%; Pred. No. 0;
tive 6; Mismatches
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NAME/KEY: CDS
LOCATION: (1) .. (3498)
NAME/KEY: misc. feature
NAME/KEY: misc. feature
LOCATION: (1102) .. (1102)
COTHER INFORMATION: n is any nucleic acid
NAME/KEY: misc. feature
LOCATION: (2650) .. (2650)
COTHER INFORMATION: n is any nucleic acid
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US-09-350-982C-4
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Patent No. 6455290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.7
Matches 3290; Conservative
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ORGANISM: Artificial
FEATURE:
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US-09-350-982C-4
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                                    1758 TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATTTAGA 1817
                                                                                   TACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGGGA 2142
                                                                                           TGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTC 2202
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ATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA
                            TGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAAGGAAAATATGA
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GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG 3438 GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG GTCTGTGGAAGAAAGAAGATACAAAGTACAGTTCGAGAGCACAGAGAGATGGAGGTCATGCAGG 3283 ACGAATGCTATTTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGATGA
1078 ACGAATGCTATTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGATGA TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTACAGAGGAGAACA GAACACCTCTGGTAGTGGAACAATTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTCA GTCTGTGGAGGAAGAAGTACAAGTTCGAGAGCACAGAGATGGAGGTCATGCAGG 258 CAGAICTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTC TTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCAC TGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACA CAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTC Sequence 1, Application US/09972115A

patent No. 6599728

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Gregg, Morin B.
APPLICANT: Mieczyalaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION UNMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
LENGTH: 4493

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LOCATION: (1)(3999) OTHER INFORMATION: NAME/KEY: misc_feature		INFORMATION: IN CO PIOVIDE ALIGHMENT. EXT. misc feature ION: (2536)(2860)
LOCATION: (1)(586) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment. NAME/KEY: misc feature	Unknown residue put	INFORMATION: Sequences not determined at this position . Unknown re INFORMATION: in to provide alignment. EEST: misc feature ION: (3163). (3163)
LOCATION: (596)(597) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	; OTHER INFORMATION: Sequences not determined at this position . Unknown residue F; OTHER INFORMATION: in to provide alignment. ; NAME/KEY: misc_feature . I.OCATTON: (1488) . (1489)
NAME TO SELECTION: (617). (617	Unknown residue put	004
NAME/KEY: misc feature LOCATION: (626)(626) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	Query Match Best Local Similarity 98.6%; Pred. No. 0; Matches 3028; Conservative 1; Mismatches 363; Indels 27; Gaps 2;
	Unknown residue put	Qy 403 AGGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAATGGTGCAAGTGTCCAAGC 462
AMAZYANIN: (638). (638). OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: 1n to provide alignment.	Unknown residue put	Oy 463 ACGTGATGATGACCCTTATTCCTCTTCATAATGCATGCTCTTTGGTCATGCTGAAGT 522
NAMEATION: (BSO_reactive LOCATION: (BSO)T. (GS4) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	QY 523 AGTCAATCTCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATAC 582
NAME/NOTION: (124). (12	Unknown residue put	Qy 583 TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGCA 642
NAMEZION: MISCLEGATURE LOCATION: (730). (730). OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	Qy 643 TGGAGCTGAGCCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC 702
NAMEATION: (764)(764). OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	Qy 703 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGTGAACTTAGAAAGTGCCAG 762
NAME ALS INTEGRATION (791). (791) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	Qy 763 GAGTGGCAATGAAAAAAAGCTCTACTCACACCATTAAATGTCAACTGCCACGC 822
NAMEAINS: miscreature LOCATION: (2148). OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	QY 823 AAGTGATGGCAGAAAGTCCATTACATTTGGCAGGATATAACAGAGTAAAGAT 882
NAMEATION: (12177). (12177) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	OY 883 TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGT 942 1152 TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGT 1211
NAME.Asi misc_teature LOCATION: (2387)(2382) OTHER INFORMATION: Sequences not determined at this position . OTHER INPORMATION: in to provide alignment.	Unknown residue put	Qy 943 ACCATTACACAATGCCTGTTCTTATGGAGTAACTGAACTGTTTGGTCAAGCA 1002
LOCATION: (2398). (2398) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	Unknown residue put	OY 1003 TGGTGCTGTGTAAATGCAATGGGCTATTCACTCCTCTTCATGAGGCAGCTTC 1062 Db 1272 TGGTGCCTGTGTAAATGCAATGGACTTGTGGCCAATTCACTCCTCTTCATGAGGCAGCTTC 1331
NAMEATION: (1846). LOCATION: (1846). OTHER INFORMATION: Sequences not determined at this position . OTHER INPORMATION: in to provide alignment. NAME/KEV. misc feature	Unknown residue put	OY 1063 TAAGAACAGGTTGAAGTATCTTCTTTTAAGTTATGGTGCAACCAAC
LOCATION: (2468)(2468) OTHER INFORMATION: Sequences not determined at this position .	Unknown residue put	Oy 1123 CAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACCACAGTTAAAAGAAAG

2263 2532 2317 2592 2377 2652		3012 2797 3072 3132 2917 3192 3037 3037 3157 3492 3492 3552
1451 1242 1511 1302 1571 1631	1422 1691 1482 1751 1542 1811 1602 1871 1662	1991 1782 2051 1842 2111 1902 2111 2022 2231 2082 2351 2082 2411 2082 2411 2202 2411 2202 2411 2202 2411
CACAATAAAAGTGCTATAGACTTGGCTCCCACACCACAGATTAAAAGAAAG	AAAGGGGAAACTCAATGAAAGACTAAAGAATTCTTGACTCTCTGCAGT AAAGGAGCAAACATCAATGAAAGACTAAAGAATTCTTGACTCTCTGCAGGT GAGAAAGCTCATAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCAGGT GAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT GAGAAAACTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGGTCTCTGGAAAATTGTTGTTGTTGTTGTTGTTGTTGTTTTTTTT	AAATTCAGAGGGAACAGATTGCTGGAAGGTGCAAAGGCTGGAGATTGGAAGATTGCAAAGGCTGGAAAGGTTGGAAAGTTGCAAAGGCTGGAAAGGTTGAAGGGTGGAAAAGGTTGAAGGGTGCAAAAAACTGTTGAAGGGTGTAAACACTGCAAGAGAATTGAAGGGGTCAAAAAACTGTTGTAACTGCAAGAGTGTCCGTGGTGGAATATCTGCTCCACTTTTTGCAGGTATAACAGAGTGTCCGTGGTGGAATATCTGCTCCACTTTTTTGCAGCTGGTATAACAGAGTGTCCGTGGTGGAATATCTGCTCCACTTTTTTGCAGCTGGTATAAAGATGAGGTGTTAAAAGATGCAGAATTGCAGAGTTTAAAAGATAAAGAGAAAAAAGAGAAAAAAAA
1392 CAATTGTCACAATAAA 1183 AGCATATGAATTTAAA 1452 AGCATAAAAACATTTAAA 1243 AATCAAAAAACATCTC 1512 AATCAAAAAACATCTC 1303 AGCATTGCATTGTGCTT 1572 AGCATTGCATTGTGCTT 1572 AGCATTGCATTGTGCTT		

3036 GCCAATGAACGAATGCTATTTCATGGGTCTCCTTTTGTGAA 3315 3GAGGACTTATTCCTTTACATAATGCAGCATCTTACGGGCA 2376 3AAGCAGCCCAAAAGGGACGAACACAGCTTTGTGCTTTGTT 2496 CCGACTCTTAAAATCAGGAAGGACAAACACCTTTAGATTT 2556 STGCTCAATGGTGTGAGAAGCCCAGAGCCACTGCAGATGC 2676 AGCCATCAAGCCTTTCTGCAGCCAGCAGTCTTGACAACTT 2736 GTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAA 2856 ATGGATATATTTGAGAGAACAGATCACTTTGGATGTATT 2916 AGTGGAACAATTCTTATAGATCTGTCTCCTGATGATAAAGA 3096 SAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCA 3156 GAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCA 3431 AGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAA 3216 -----GGAAAGATACACTCACCGGAGAAAGAAGTTTC 3255 AATTTAGAAGTTGCAGAGTATTTGTTACAACACGGAGCTGA 2316 AGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCC 2616 3TGCTCAATGGTGTGGAGAGCCCAGGAGCCACTGCAGTGC 2951 CTGTCTTCAGTAGTTAGTTCAAGTGGAACAGAGGGTGCTTC 2796 GTTCCAGGAGTAGATTTTAGCATAACTCCAATTCGTAAGGAA 3131 CTAATAAAGTATAATGCATGTGTCAATGCCACGGACAAATG SAGAGACTTATCTCCGGACAACAAGGTCTTAACCCATATTT

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NAME/KEY: misc feature
LOCATION: (125)...(125)
OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc feature
LOCATION: (293)...(293)
OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
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                      3612 TGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGC 3671
                                                                                                         3436 AGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGCTGCT 3495
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                                                                                                                                                                                                                                                                              CITITIGECGGGTAACCITIGGGAAAGTCITICCTGCAGITCAGTGCAATGAAAATGGCACA 3851
                                                                                                                                                                                                                                                                                                                                          TTCTCCTCCAGGTCATCACTCACTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGC 3615
                                                                                                                                                                                                                                                                                                                                                                                                                           CTITICCCGGGTAACCTIGGGAAAGICTITCCTGCAGITCAGIGCAATGAAAAIGGCACA 3555
                                                                                                                                                                                                                                                                                                                                                                               3852 Trcrccrccaggrcarcacrcagrcacregraggcccagrgraaarggccragcarragc 3911
                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGAGGCCTGAAGGTATGGTCGATGGATAATAGTTATTTTAAGAAACTAATTCCACTG 3735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3972 TATGAGGCCTGAAGGTATGGTCGATGATAATAGTTATTTTAAGAAACTAATTCCACTG 4031
TGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGC 3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4032 AACCTAAAATCATCAAAGCAGCAGTGGCCTCTACGTTTTACTCCTTTGCTGAAAAAA 4090
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LOCATION: (1)..(3801)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
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Patent No. 6599728

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gerog, Morin B.
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
SEQ ID NOS: 64
SOOTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 4297
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ORGANISM: Homo sapiens
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put put put LOCATION: (682).. (682) OTHER INFORMATION: Sequences not determined at this position . Unknown residue put OTHER INFORMATION: in to provide alignment. Unknown residue put Unknown residue Unknown residue Unknown residue residue Unknown NAME/KEY: misc feature COTHER INFORMATION: Sequences not determined at this position . Un) OTHER INFORMATION: Sequences not determined at this position . Un) OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc feature (6147 . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (614) . (619 OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc. feature
LOCATION: (341)...(341)

OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc. feature
LOCATION: (378)...(378) LOCATION: (378)...(378)

OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: (415)...(415)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc feature
LOCATION: (432)...(432) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc. feature
LOCATION: (496)...(496)...
OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.

LOCATION: (517)...(517) LOCATION: (517)...(517)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: 10.40
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: 1n to provide alignment.
NAME/KEY: misc feature
LOCATION: (533)...(533)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment. OTHER INFORMATION: Sequences not determined at this position .

OTHER INFORMATION: In to provide alignment.

NAME/KEY: misc feature
LOCATION: (637)..(637). NAME/KEY: misc_feature
LOCATION: (680)...(680)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (682)...(682) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc_feature
LOCATION: (643)..(643) LOCATION: (643). OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment. LOCATION: (432)..(432) OTHER INFORMATION: Sequences not determined at this position OTHER INFORMATION: in to provide alignment. NAME/KEY: misc feature LOCATION: (459)..(459)

Unknown residue put Unknown r
n residue 2; 2; 2; 535 535 595 655
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PRANTION: Sequences not determined at this position . Unknow PRANTION: 10 to provide alignment. (1977). (1971). (1977). (1977). (1977). (19
OTHER INFORMATION: Sequences not OTHER INFORMATION: in to provide NAME/KEY: misc_feature COCATION: (1971)(1971) CTHER INFORMATION: in to provide CTHER INFORMATION: in to provide COTHER INFORMATION: in to provide COCATION: (2000)(2000) COTHER INFORMATION: in to provide COCATION: (2180)(2180) COTHER INFORMATION: in to provide COCATION: (2180)(2180) COTHER INFORMATION: in to provide COCATION: (2180)(2180) COTHER INFORMATION: in to provide COCATION: (2205)(2205) COCATION: (2207)(2201) COCATION: (2207)(2200) COCATION: (2207)(2200) COCATION: (2207)(2200) COCATION: (2207)(2200) COCATION: (2207)(2200) COCATION: (2207)(2200) COCATION: (2200)(2200) COCATION: (2200)(2200) COCATION: (2200)(2200) COCATION: (2200)(2200) COCATION: (2200)(2200)

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                                                                ATGGACATAGGCACAAACTAAAAAGTTTCGAGAGACTTATCTCCGGACAACAAGGTC
                                                                                                     TTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAGATCTGTCTC
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                                                       AACATGGAGCAGTAATTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAG
                                                                                                                                            CAGCADAAGGAAAATATGAAATTTGCABAACTTCTGCTCCAGCATGGCAGGACCCCTACAA
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 GAGACATTGAAGGGCGTCAGTCTACACTTTCATTTTGCAGCTGGGTATAACAGAGTGT
                              CCGTGGTGGAATATCTGCTACAGGATGGAGCTGATGTGCATGCTAAAGATAAAGGGGCC
                                                                                                                                                                        AAAAAACAGGGATGGAAATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTC
                                                                                                                                                                                                              AAGATCTGCTTAGGGGAGATGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCA
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ATTCTCCTCCAGGTCATCACTCACTGGTAGGCCCCAGTGAAATGGCCTAGCATTAG TTATGAGGCCTGAAGGTATGGTCGATGAATAGTTATTTAAGAAACTAATTCCACT TCTTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCAC TTATGAGGCCTGAAGGTATGGTCGATGGATAAATAGTTATTTTAAGAAACTAATTCCACT Sequence 1, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

us-10-616-101-1.rni

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 891; Indels
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version:
               4th Floor
                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-230 CIP1
RELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
              I: 411 Hackensack Avenue,HackensackNew Jersey
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 72.3
Matches 2395; Conservative
ADDRESSEE: Klauber &
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                          CITY: Hackense
STATE: New Jex
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
FLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09841835;
Patent No. 6506897;
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Suan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO T
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack
CITY: Hackensack
STATE: New Jersey
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3936 ATGAAGCCAGAAG 3948
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2217 AGGCATGGGGCTTCTGTCAATGTGGCGGACTTATGGAAATTTACCCCTCTCCATGAAGCA 2276
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Pred. No. 0;
0; Mismatches 891; Indels
                                                                       600-1-230
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                       NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REPRENCE/DOCKET NUMBER: 600-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-343-1684
                                                                                                            TELEFAX: 201-343-1684
TELEX: 13321
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.3
Matches 2395; Conservative
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Sequence 7, Application US/09972115A
Patent No. 6599728
GENERAL INFORMATION:
APPLICANT: Geron Corporation
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                                                                                   CCATCTGCTCTGCCTCTTACAAGCCTCAAGTGCTCAATGGTGTGAGAAGCCCAGGA 2662
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2457 AGAGTGCAGAAGCTCTGTACCCCAGAGAATATCAACTGCAGAGACACCCCAGGGCAGAAAT 2516
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47.8%; Score 1813.4; DB 3; Length
Best Local Similarity 72.3%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 891; Indels APPLICANT: Gregg, Morin B.
APPLICANT: Gregg, Morin B.
APPLICANT: Walter Funk D.
APPLICANT: Walter Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REPERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT PILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1

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2783 ACAGAGGGTGCTTCCAGTTTGGAGAAAAG-----GAGGTTCCAGGAGTAGATTTTAGC 2836
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Search completed: December 18, 2006, 16:38:15 Job time : 662.368 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

December 18, 2006, 17:00:29; Search time 3854.36 Seconds (without alignments) 12104.784 Million cell updates/sec Run on:

US-10-616-101-1 3797 Title: Perfect score:

1 ctttgaagacactggatttc.......sctttgctgaaaaaaaaaa 3797

Sequence:

18892170 seqs, 6143817638 residues Searched:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_NA_Main:

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 14, Appl	Sequence 100, App	Sequence 106, App	Sequence 134, App	Sequence 132, App	Sequence 556, App	11, A	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 92, Appl	Sequence 88, Appl
ID	US-10-616-101-1	US-10-616-101-2	US-09-972-115A-5	US-10-163-587A-14	US-10-199-937-100	US-10-199-937-106	US-10-199-937-134	US-10-199-937-132	US-10-302-172-556	US-09-849-602-11	US-10-898-653-5	US-09-509-196A-1	US-10-199-937-1	US-09-972-115A-1	US-09-972-115A-3	US-10-199-937-92	US-10-199-937-88
Length DB	3797 10	16 10	4275 3	78 6	27 7	06 7	92 7	02 7	75 8	6018 3	89 10	1400 3	08 7	93 3	297 3	71 7	53 7
Leng		38	42	57	41	44	49	20	50	9	61	34	35	44	42	2971	33
% Query Match	100.0	89.4	89.2	89.2	89.2	89.2	89.2	89.2	89.2	89.2	89.2	86.8	86.8	78.2	78.2	64.3	64.3
Score	3797	3393.4	3388.8	3388.8	3387.2	3387.2	3387.2	3387.2	3387.2	3387.2	. 3387.2	3297	3296.2	2969.6	2968.2	2439.8	2439.8
Result No.	-	7	٣	4	S	9	7	8	6	10	11	12	13	14	15	16	17

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90,	Sequence 3, Appli	Sequence 1, Appli	7,	Sequence 342, App	•	9	98,	Sequence 9, Appli	Sequence 340, App			Sequence 138, App	m	Sequence 40, Appl	Sequence 40, Appl	Sequence 341, App	Sequence 9472, Ap	Sequence 45, Appl	Sequence 10, Appl	Sequence 2223, Ap	Sequence 5, Appli		Sequence 623214,	Sequence 623214,	σ	Sequence 17041, A	4
7 US-10-199-937-90	7 US-10-199-937-3	3 US-09-841-835-1	3 US-09-972-115A-7	7 US-10-252-157-342	3 US-09-841-835-7	10 US-10-898-653-4	7 US-10-199-937-98	3 . US-09-841-835-9	8 US-10-276-774-340	7 US-10-199-937-177	7 US-10-199-937-159	7 US-10-199-937-138	13 US-11-097-143-9473	3 US-09-964-899-40	10 US-10-975-523-40	7 US-10-252-157-341	13 US-11-097-143-9472	7 US-10-199-937-45	3 US-09-972-115A-10	6 US-10-106-698-2223	7 US-10-199-937-5	7 US-10-181-447A-11	4 US-09-925-065A-623214	5 US-09-925-065A-623214	3 US-09-972-115A-9	3 US-09-918-995-17041	7 US-10-199-937-41
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62.1	47.8	47.8	47.8	40.4	38.2	38.2	35.8	34.2	32.7	30.8	28.6	26.6	26.6	26.2	26.2	20.9	19.7	15.1	13.7	12.1	12.1	10.5	10.4	10.4	10.0	9.7	9.5
2357.8	1813.4	1813.4	1813.4	1533.8	1449.6	1449.6	1359.4	1297.8	1240.4	1168.4	1084.8	1008.8	1008.8	994	994	794.4	748.6	574	518.4	459	459	396.8	393.6	393.6	380.4	368	359.6
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ALIGNMENTS

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APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
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APPLICANT: Au, Xiang
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APPLICANT: Mund, Betty
APPLICANT: Ossovskaya, Valeria
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
FILE REFERENCE: RIGL-010CIP3
CURRENT PILING DATE: 2003-07-08
FRIOR APPLICATION NUMBER: US 09/843,159
FRIOR PELING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
PRIOR PELING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO.1
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Sequence 1, Application US/10616101 Publication No. US20050074825A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 3797; Conservative
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Sequence 5, Application US/09972115A
Publication No. US20030032769A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Mieczyslaw, Piatyszek A.
APPLICANT: Mieczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SEQ ID NO S: 64
SEQ ID NO S: LENGTH: 4275
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; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5
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Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
TITLE OF INVENTION: TANTRASE2 WATERIALS AND FILE REPERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT APPLICATION NUMBER: US/09/606,035
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR PELING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 106
LENGTH: 4406
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US-10-199-937-106
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Pred. No. 0;
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                                                 Query Match
Best Local Similarity 99.9%;
Matches 3389; Conservative
; TYPE: DNA; ORGANISM: Homo sapiens; FEATURE: ; NAME/KEY: CDS; LOCATION: (2). (3787)
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Squence 134, Application US/1019937

Publication No. US2003019073941

GENERAL INFORMATION:

APPLICANT: Christenson, Erik

APPLICANT: DeMaggio, Anthony J.

APPLICANT: Defiden, Phylis S.

APPLICANT: McElligott, David L.

ITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS

FILE REFERENCE: 27866/36559

CURRENT APPLICATION NUMBER: US/10/199,937

CURRENT PILING DATE: 2002-07-22

PRIOR PILING DATE: 2000-06-28

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 178

SSCTUMBER: PRECHING VET: 1.00 174

SEC ID NO 134

LENGTH: 4992
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US-10-199-937-134
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT APPLICATION NUMBER: US/09/606,035
FRIOR APPLICATION NUMBER: US/09/606,035
FRIOR FILING DATE: 2000-06-28
FRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: 5002
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; LOCATION: (229)..(4383)
US-10-199-937-132
                                                                                                                                      TYPE: DNA
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Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllas S.
APPLICANT: MCGlidman, Phyllas S.
APPLICANT: MCBILIGOTE, David L.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
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                                                                                          JAPPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Pan
FILE REPERENCE: LOGGI/1105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 11
                                                US-09-849-602-11
; Sequence 11, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapien
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89.2%; Score 3387.2;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches
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Publication No. US20050143370A1;
GENERAL INFORMATION:
JAPPLICANT: Helleday et al
TITLE OF INVENTION: Therapeutic Compounds;
PILE REFERENCE: J660-046;
CURRENT APPLICATION NUMBER: US/10/898,653;
CURRENT FILING DATE: 2004-07-23;
NUMBER OF SEQ ID NOS: 6
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US-10-898-653-5
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GRNEKAL INFUGUATION:

APPLICANT: DALY, Roger J.

APPLICANT: BULY, Roger J.

APPLICANT: SUTHERLAND, Robert L.

ITILE OF INVENTION: A Potential Effector for the Grb7 Family of Sign TITLE OF INVENTION: Proteins

FILE REFERENCE: 1871-129

CURRENT APPLICATION NUMBER: US/09/509,196A

CURRENT APPLICATION NUMBER: DO00-03-23

PRIOR FILING DATE: 1997-09-23

PRIOR FILING DATE: 1998-09-23

PRIOR FILING DATE: 1998-09-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 1

LENGTH: 3400

TYPE: DNA

TYPE: DNA

ONGANISM: Homo sapiens
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Pred. No. 0;
0; Mismatches 10; Indels
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1202 CACTCGTIGCTGCAAGCTGCACGAGAAGCTGATGTTACTCGAATCAAAAAACATCTCTT 1261

661 GCTATAGACTTGGCTCCCACACCACAGTTAAAAGAAAGATTAGCATATGAATTTAAAGGC 720

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US-09-509-196A-1; Sequence 1, Application US/09509196A; Patent No. US20020037582A1

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1167 1002 1062 1122 1242 1047 1362 1422 1227 1482 1287 1542 1602 1347 1467 1407 447 702 762 822 942 747 807 867 927 507 567 627 882 687 388 TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGCA 808 TGGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTC TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC 703 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACCCATTAAATGTCAACTGCCACGC TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCCATGCTAAAGATAAAGGTGATCTGGT 1183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGC AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGGAGATATAACAGAGTAAAGAT AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCA 1003 TGGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTC AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG 1168 GCTAAGAAAAGGAAGCAAACATGAAAGAAGACTAAAGAATTCTTGACTCCTCTGCAGG TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGT GCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT 1543 ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCTTCAGGG 1423 GGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGGT

	2983 AAITAAAGGAGTCGAGAGACITAICTCCGGACAACAAGGTCTTAACCCAIATTTAACITT 3042 2788 AAITAAAGGAGTCGAGAGACTTAICTCCGGACAACAAGGTCTTAACCCAIATTTAACITT 2847 3043 GAACACCTCTGGTAGTGGAACAATTCTTAIAGATCTCTCTGATGATAAAGAGTTTCA 3102 2848 GAACACCTCTGGTAGTGGAACAATTCTTAIAGATCTGTCTCCTGATGATAAAGAGTTTCA 2907 3103 GTCTGTGGAAGAAGAACAATTCTTAIAGATCTGTCTCCTGATGATAAAGAGTTTCA 2907 3103 GTCTGTGGAAGAAGAACAATTCTTATAGATCGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	163 TGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTATG 3222		268 CAGAICTIGITACATTIGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTC 523 TTTCCTGCAGTTCAGTGCAAATGACAATTCTCCTCCTCCAGGTCATCAGGTCAC 528 TTTCTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3643 GGCTTATCCTGAGTATTAATTACTTACCACATTATGAGGCTGAAGGTATGGTCGATGG 3702 	RESULT 14 US-09-972-115A-1 ; Sequence 1, Application US/09972115A ; Publication No. US20030032769A1 ; GENERAL INFORMATION:
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	ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTTGTACCTTTGCACAATGC ATGTTCTTATGGACATTATGAGTTGCAGAACTTCTTGTTAAACATGGAGCGGTAGTTAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1828 AATTIGCAAACTICTGCTCCAGCATGGAGCCCTACAAAAAAAAAA	TCCTGATAAATTGCCGCGATACCCAGGCTCTTCAACACTTTAGC AGCTGGTTAATAATTTAGAAGTTGCAGGGTATTTGTTACAACACGGAGCTGATTAGC AGCTGGTTATAAATTAAAT	2188 TOTAGCACTCTACTAATAAAGTATAATGCATGCACCACCACCACAATGCACTT 2247 2188 TOTAGCACTCTACTAATAAAGTATAATGCATGTGTCCAATGCCACCACAAATGGCCTTT 2247 2443 CACACCTTTGCACGAAGCAGCCCAAAAGGGACGAACACAGCTTTGTTGCTTAGTTGCTAGC 2502 2248 CACACCTTTGCACGAAGCAGCCCAAAAGGGACGAACACAGCTTTGTTGTTGTTGTTGCTAGC 2307 2503 CCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGAACAACCCTTTAGATTTAGTTTC 2562 2308 CCATGGAGCTGACCCGACTCTTAAAAATCAGGAAGAACAACCCTTTAGATTTAGTTTC 2367		2683 TTCAGGTCCATCTAGCCCATTCTGCAGCCAGCCAGCAGCAGTCTTGACAACTTATCTGG 2742

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; LOCATION: (3488)..(3499)
; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
; OTHER INFORMATION: in to provide alignment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 AGGTTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAATGGTGCAAGTGTCCAAGC
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NAME/KEY: misc feature
LOCATION: (2536)
OTHER INFORMATION: Sequences not determined at this position. I
OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc feature
LOCATION: (3163)
OTHER INFORMATION: Gaquences not determined at this position.
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OTHER INFORMATION: in to provide alignment.
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LOCATION: (2398)..(2398)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
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LOCATION: (2468). (2468).
OCHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (2493). (2493).
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LOCATION: (2466)..(2466).
OTHER INFORMATION: Sequences not determined at this position
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OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: in to provide alignment.

LOCATION: (637)...(634)
OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: in to provide alignment.

NAME/KEY: misc_feature
LOCATION: (724)...(724)
OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: in to provide alignment.

NAME/KEY: misc_feature
LOCATION: (730)...
OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: Sequences not determined at this position . Unknown residue put OCHER INFORMATION: in to provide alignment.
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LOCATION: (596)...(597)
OTHER INFORMATION: Sequences not determined at this position. Unknown residue put
OTHER INFORMATION: in to provide alignment.
LOCATION: (621)...(621)
OTHER INFORMATION: Sequences not determined at this position. Unknown residue put
OTHER INFORMATION: in to provide alignment.
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LOCATION: (2177)..(2177)
OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
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LOCATION: (764).
OTHER INFORMATION: Sequences not determined at this position . Unknown residue put
OTHER INFORMATION: in to provide alignment.
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LOCATION: (1). (586)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
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LOCATION: (626). (626)
OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc feature
LOCATION: (629)...(629)
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OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
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APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Malex, Funk D.
APPLICANT: Malex, Funk D.
APPLICANT: Maczyalaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFRENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/129,577
PRIOR FILING DATE: 1090-04-10
PRIOR PILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)..(3999)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         3376 IGGCATTITATTTTGCTGAAAACTCTTCCAAAAGCAATCAATATGTATATGGAATTGGAGG 3435
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                                                                                                                                                                            3157 TGCAGGTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAA
                                                                                                                                                      -----GGAAAGATACACTCACCGGAGAAAAGAAGTTTC
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APPLICANT: Greeg, Morin B.
APPLICANT: Greeg, Morin B.
APPLICANT: Walter, Funk D.
ITILE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/129,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR PLING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 3
LENGTH: 4297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09972115A Publication No. US20030032769A1 GENERAL INFORMATION:
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                                                 NAME/KEY: misc feature
LOCATION: (1) ... (1)
COTHER INFORMATION: Sequences not determined at this position. U
COTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
COTHER INFORMATION: in to provide alignment.
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COTHER INFORMATION: in to provide alignment.
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OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCARION: (632)..(632)
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NAME/KEY: misc_feature
LOCATION: (496).

OTHER INFORMATION: Sequences not determined at this position OTHER INFORMATION: in to provide alignment.
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LOCATION: (341). (341)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (378). (378)
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NAME/KEY: misc feature
LOCATION: (4327. (432)
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LOCATION: (517)..(517)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
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LOCATION: (534). (534)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
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LOCATION: (551)..(553)..
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
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LOCATION: (562)..(562)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
LOMANE/KEY: misc_feature
LOCATION: (614)..(614)
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LOCATION: (415)..(415)
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LOCATION: (619)..(619)
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LOCATION: (459)..(459)
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LOCATION: (1)..(3801)
OTHER INFORMATION:
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	504 CTTTTGGTCATGCTGAAGTGAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTC 563	564 GAGATAATTGGAATTATACTCCTCCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTT 623 	624 GCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACGG 683 	684 CATTGGATTTAGCAGATCCATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGA	744 AACTCTTAGAAAGTGCCAGGAGTGGCAATGAAGAAAAATGATGGCTCTACTCACCAT 803 	804 TAAATGTCAACTGCCACGCAAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAG 863 	864 GATATAACAGAGAAAAATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTA 923 	924 AAGATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAA 983 	984 CTGAACTTTTGGTCAAGCATGGTGCTGTGTAAATGCAATGGACTTGTGGGCAATTCACTC 1043 	1044 CICTTCATGAGGCAGCTICTAAGAACAGGGTTGAAGTATGTTCTCTTCTC	1104 GTGCAGACCCAACACTGCTCAATTGTCACAATAAAGTGCTATAGACTTGGCTCCCACAC 1163 	1164 CACAGTTAAAAGAAAGATTAGCATATGAATTTAAAGGCCACTGGTTGCTGCAAGCTCCCC 1223 	1224 GAGAAGCTGATGTTACTCGAATCAAAAACATCTCTCTGGAAATGGTGAATTTCAAGC 1283 	1284 ATCCTCAAACACATGAAACACCATTGCATTGTGCTGCTGCATCTCCATATCCCAAAAGAA 1343 	1344 AGCAAATATGTGAACTGTTGCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAAT 	1404 TCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGG 1463 1496 TCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGG 1555	1464 TGAAACATGAAGCAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAG 	1524 CIGCATATTGTGGTCATCTACAAACCTGCCGCCTACTCGAGCTATGGGTGTGATCCTA 1583
qq	& 8	è d	& 8	& 8	δ P	& g	<u>ራ</u>	è a	B &	& 8	ъ 8	& 8	ъ д	B &	& 8	상 원	P &	ò
Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put		4 n	
TION: Sequences not determined at this position . TION: in to provide alignment. c feature	ION: (643)(643) INFORMATION: Sequences not determined at this position . INFORMATION: in to provide alignment.	Mat: WINE_Learure ION: (680). (680) INFORMATION: Sequences not determined at this position . INFORMATION: in to provide alignment.	NAMES AST: MISC. Leacure LOCATION: (682)(682). OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	or reature $11(713)$ and determined at this position . TION: in to provide alignment.	NAME/KEY: misc feature LOCATION: (1971)(1971) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	TION: (2000)	MAX: MISS reacure LON: (2175)(2175) INFORMATION: Sequences not determined at this position . INFORMATION: in to provide alignment.	юнн	NAME/KET: MISC reacure LCATION: (2205)(2205) OTHER INFORMATION: Sequences not determined at this position . OTHER INFORMATION: in to provide alignment.	misc reature (2221)(2221). DRWATION: Sequences not determined at this position . DRWATION: in to provide alignment.	teature 89). (2289) TION: Sequences not determined at this position . TION: in to provide alignment.	 _reature 16](2316) TION: Sequences not determined at this position . TION: in to provide alignment. 	<pre>c reature 59)(267)0267)</pre>	L H H	"_reature 91). (2291) TION: Sequences not determined at this position . TION: in to provide alignment.	18.2%; Score 2968.2; DB 3; Length 4297. Larity 88.3%; Pred. No. 0; Concaryetive 7. Migmatches 31: Indels 12.	TITATCATTAAGGITITGGGGGGAAAGACGIAGITGAATAI	4/4 ATGGTGCAAGTGTCCAAGCACGTGATGAGGGGCCTTATTCCTCTTCATAATGCATGC
OTHER INFORMATION: OTHER INFORMATION: NAME/KEY: misc fea	LOCATION: (643)(6 OTHER INFORMATION: OTHER INFORMATION:	MANDA MET : MILEC LEGILLE LOCATION: (680) OTHER INFORMATION: SEG OTHER INFORMATION: in in	CATION: (682 THER INFORMATINES INFORMATINES INFORMATINES	NAME/KEY: MISC TEACUTE LOCATION: (711)(713) OTHER INFORMATION: Seq	AME/KEY: misc CCATION: (197 THER INFORMAT	NAME/KEY: M18C E LOCATION: (2000) OTHER INFORMATIO	NAME/AEI: MIBG C LOCATION: (2175) OTHER INFORMATION OTHER INFORMATION	NAME/KEY: MIBG LOCATION: (216 OTHER INFORMAT OTHER INFORMAT	NAME/KEY: MISC LOCATION: (220 OTHER INFORMAT	NAME/KEY: MIBC FERRILLOCATION: (2221). OTHER INFORMATION: OTHER OTHER	NAME AND THE STATE OF THE STATE	NAME/KKY: MISC Feature LOCATION: (2316)(2316) OTHER INFORMATION: Seque OTHER INFORMATION: in to	NAME/KEY: MISC Feature LOCATION: (2359)(2674) OTHER INFORMATION: Seque OTHER INFORMATION: in to	NAME/KEY: MISC_ICAT LOCATION: (2977) OTHER INFORMATION: OTHER INFORMATION:	NAME/KEY: MIBG TE LOCATION: (2291). OTHER INFORMATION OTHER INFORMATION 9-972-115A-3	atch cal Simi	384 CCC	47.9 CCCC

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1516 CTGCATATTCTGGTCATCAACCTTCCCCCCTACTCCTGAGCTAATGGATCCTAACCCCCAAC 1675 1564 ACATTATTATCCTTCACGCCTTTAACTCTTCTTCACGCCACCCTAACTCTCAACACCCCCCCC	2544 2633 2604 2693

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| Search completed: December 18, 2006, 21:41:00 Job time : 3863.36 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

December 18, 2006, 17:00:26 Run on:

; Search time 754.113 Seconds (without alignments)
10686.273 Million cell updates/sec

US-10-616-101-1 3797 Title: Perfect score:

1 ctttgaagacactggatttc......3797 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

3026960 seqs, 1061187768 residues Searched:

6053920 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA New: Database :

1: FEMC_Celerra_SIDS3/ptodata/l/pubpna/US09_NEW_PUB.seq:*
2: AEMC_Celerra_SIDS3/ptodata/l/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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	ä	23602,	23750,	29428,	22929,	251004,	311521,	99554,	152365,	189602,	55144,	217436,	165504,	244089,	116071,	158235,	221377,	286109,	337538,	396481,	467527,	379999,	463378,
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence
	ΩI	US-11-266-748A-23602	US-11-266-748A-23750	US-11-266-748A-29428	US-11-266-748A-22929	US-11-266-748A-251004	US-11-266-748A-311521	US-11-266-748A-99554	US-11-266-748A-152365	US-11-266-748A-189602	US-11-266-748A-55144	US-11-266-748A-217436	US-11-266-748A-165504	US-11-266-748A-244089	US-11-266-748A-116071	US-11-266-748A-158235	US-11-266-748A-221377	US-11-266-748A-286109	US-11-266-748A-337538	US-11-266-748A-396481	US-11-266-748A-467527	US-11-266-748A-379999	US-11-266-748A-463378
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æ	Query Match	89.2	89.2	47.8	47.3	17.5	17.5	15.0	15.0	14.1	14.1	14.1	13.6	13.6	13.3	13.3	13.3	13.3	13.3	13.3	13.3	8.9	8.0
	Score	3387.2	3387.2	1813.4	1794.8	663.8	663.8	570	570	535.6	533.6	533.6	515.6	515.6	503.2	503.2	503.2	503.2	503.2	503.2	503.2	336.8	336.8
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337 AGGITITIGGGCGGAAAGACGTAGTIGAATATITIGCTICAGAATGGTGCAAATGTCCAAGC 396

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Sequence 8589, Ap Sequence 3203, Ap Sequence 272728,	Sequence 333245, Sequence 380066,	Seguence 463445, Seguence 174653,	Sequence 246075, Sequence 56688, A	3160		Seguence 32152, A	Sequence 32784, A	Sequence 25093, A	Sequence 23775, A	Sequence 3622, Ap	Sequence 22278, A	Sequence 3623, Ap	Sequence 1815, Ap	Seguence 1819, Ap	Sequence 2096, Ap	Sequence 7246, Ap	Sequence 65708, A
US-11-266-748A-8589 US-10-513-369-3203 US-11-266-748A-272728	US-11-266-748A-333245 US-11-266-748A-380066	US-11-266-748A-463445 US-11-266-748A-174653	US-11-266-748A-246075 US-11-266-748A-56688	US-10-834-268-3160	US-11-293-697-794	US-11-266-748A-32152	US-11-266-748A-32784	US-11-266-748A-25093	US-11-266-748A-23775	US-11-216-545-3622	US-11-266-748A-22278	US-11-216-545-3623	US-10-374-780A-1815	US-10-374-780A-1819	US-11-371-354-2096	US-11-371-354-7246	US-11-371-354-65708
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289.8 271.8 267	267 211.8	211.8	112	94	8.06	90.8	90.8	83.8	82.2	81.2	80.2	79.6	79.6	77.8	77.4	77.4	77.4
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ALIGNMENTS

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403 AGGITITIGGGCGGAAAGACGIAGIIGAAIAITITGCIICAGAAIGGIGCAAGIGICCAAGC 462
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                                                                                                                         APPLICANT: Harkin, Faul
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Mulligan, Karl
TITE OF INVENTION: Transcriptome Microarray Technology and
TITE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
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PRIOR PRILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
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99.9%; Pred. No. 0;
tive 0; Mismatches
Sequence 23602, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity 99.9
Matches 3389; Conservative
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US-11-266-748A-23602
                                                                                                           APPLICANT: Harkin, Paul
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		ATTAGGTAATTCAGAGGCAGACAGACAATTGCTGGAAGCTGGAAAGGTGGAGATGTCGA 	aactgtaaaaaactgtgtactgttggggggtgcaactggaggacttgaagggggggg	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGACTGTCGGTGGTGGAATATCTGCT	ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGAGGCCTTGTACCTTTGCACAATGC	ATGITCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTAA	TGTAGCTGATTTATGGAAATTTACACCTTTACATGAACCAGCACCAAAAGGAAAATATGA 	AATTTGGAACTTCTGCTCCAGGTGGTGGTGCACCTTACCAAAAAAAA	TACTCCTTTGGATCTTGTTAAAGATGGAGATAAGATATTCAAGATCTGCTTAGGGGAGA 	TGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAAGTGAAGAAGTTGTCTTC 	TCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGA(CATTCAACATTTAGATTTAGG 			2383 TGTAGCAGCTCTACTAATAAAGTATAATGCATGGTCAATGCCACGGACAAATGGGCTTT 2442 	2443 CACACCTITGCACGAAGCAGCCCAAAAGGACGAACACAGCTITGTGCTITGTTGCTAGC 2502 	2503 CCATGGAGCTGACCCGACTCTTAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2562 	2563 AGCGGATGATGATCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTTTG 2622 1	2623 TTACAAGCCTCAAGTGCTCAATGGTGTGAGAAGCCCAGGAGCCACTGCAGATGCTCTCC 2682
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463 ACGTGATGATGGGGGCCTTATTCCTCTTCATAATGCATGC	AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATACCAATCTCCTTTTGCGACATGSTGCAGACCCCAATGCTCGAATATTGGAATTATATACA	H—H	TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC 	103 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTTTAGAAAGTGCCAG 762 	763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGC 822 	823 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGGAGATATAACAGAGTAAAGAT 882 	883 TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGT 942 	943 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCA 1002 	1003 TGGTGCCTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTC 1062 	TAAGAACAGGGTTGAAGTATGTTCTTTCTCTTAAGTTATGGTGCAGACCCA 	CARTIGICACAATAAAGIGCIATAGACITGGCICCCACACCACA	1183 AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG 1242 	ANTCADADADA CATCTCTCTCGDADATGGTGDATTTCDAGCATCCTCDADCCACTGDADACACACACACACACACACACACACACACACACACAC	AGCATTGCATTGTGCTGCTGCTGCTGCTCCATATCCCAAAGAAAG	GCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT	GCCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAAAGTGACGTGAAAGGT 	TAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATCT	1417 TARTGCTCTGGGATARTCTTGGTCAGACTTCTCTACAGAGCTGCATATTGTGGTCATCT 1478 1543 ACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATGTCCTTCAGGG 1602

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0
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
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                         3763 CCTCTACGTTTTACTCCTTTGCTGAAAAAA 3794
                                                3697 CCTCTACGTTTTACTCCTTTGCTGAAAAAAA 3728
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99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                        ; Sequence 23750, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.9
Matches 3389; Conservative
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; ORGANISM: Homo Sapiens
US-11-266-748A-23750
                                                                                                                                             RESULT 2
US-11-266-748A-23750
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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US-11-266-748A-29428
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Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karlick

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

CURRENT APPLICATION WUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2
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                                                                                                                                                            AGATTGATGTTTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAG 671
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                                                                62 ATAATGCCTGTTCTTTTGGCCATGCTGAGGTTGTGAGTCTGTTATTGTGCCAAGGAGCTG 121
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    3516 GAGGAGAATCACAACCATCACAATGAGCGCATGTTGTTTCATGGTTCTCCTTTCATTAAT 3575
                                                                                GGCATTTATTTTGCTGAAACTCTTCCAAAAGCAATCAATATGTATATGGAATTGGAGGA 3436
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                              GCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGCT
                                              3557 TCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCT
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Best Local Similarity 72.5
Matches 2365, Conservative
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CORGANISM: Homo Sapiens
US-11-266-748A-22929
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09 2652 GAAGCCCAGGAGCCACTGCAGTCCTTCAGGTCCATCTAGCCCATCAAGCCTTT 2711	Qy 2826 TAGATITTAGCATAACTCAATTCCTAAGGAATCTTGGACCTTGAGCACCTAATGGATATAT 2885 Db 2381 TTGACATGAATATCAAAAAGCCTTGGCCTTGACCTTCGGGATATCT 2440 Qy 2886 TTGAGAGAACAACAACAACAATTGATTAGTTGAGATGGGGCACAAGGAGCTGAAGG 2945 Db 2441 TTGAAACAGAATGACTTGGATGTTTGGTTGGCTGATAGGGTCATGAAGG 2500	2946 AGATTGGAATCATGGTTATGGACATAGGCACAACTAATTAAAGGAGTCGAGAGACTTA	Db 2621 TTTTGCTGGATCTTGCTCCAGAAGATAAGAATTATCAGTCAG		Db 2921	Oy 3546 AAATGGCACTTCTCCTCCAGGTCATCACTCAGTCAGGGCCCAGTGTAAATGGCC 3605 10. AAATGGCACCACGCGCCTCCAGGCACCACTCAGTCATTGGTAGACCGAGCGTCAATGGGC 3160 310. AAATGGCCACGCGCCTCCAGGGCACCACTCAGTAGTTGGTAGACCGAGCGTCAATGGGC 3160 Oy 3606 TAGCATTAGCTGATATTACAGAGGAGAACAGGCTTATCCTGAGTATTTAATTA 3665 Db 3161 TGGCATATGCTGATATTACAGAGGAGAACAGGCATACCTGAGTATTTAATTA 3665 Oy 3666 CTTACCAGATATGAGCCTGAAG 3689 Db 3221 CTTACCAGATCATGAAGCCAGAAG 3244
CTTTGCATAGAGCCGCCCTAGCAGGCCACCTGCCGCCCTCCTGCTGAGTTACG 1141 GGTGTGATCCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGATTACG 1141	CAAA 1321 GGGT 1811 GGCT 1381 AAAG 1871 AAAG 141	ATAAAGGAGGCCTTGTACCTTTGCACAATGCATGTTTTTGGACATTATGAAGTTGCAG 1931		AAGG 1741 ACCC 2231 ACCC 1801 ACCC 1801 ACCC 1801 CCTT 2351		2041 2531 2101 2591 2651 2066

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NUMBER: Patence
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VS-11-266-748A-251004

Sequence 251004, Application US/1126678BA

Publication NO. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Wulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58915-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR PRING DATE: 2004-11-03

PRIOR PLING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR PILING DATE: 2004-03-14

PRIOR PILING DATE
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Best Local Similarity 99.0
Matches 668; Conservative
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US-11-266-748A-251004
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                                                                                                                                                                                                      900
                                                                                                                                                                                                                                                                                                               601 CAAGGTCTTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAGAT 660
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2897 CAGATCACTTTGGATGTATTAGTTGAGATGGGGCCACAAGGAGCTGAAGGAGATTGGAATC
                                                                                                                                     2957 AATGCTTATGGACATAGGCACAAACTAAATTAAAGGAGTCGAGAGACTTATCTCCGGGACAA
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                                       481 CAGATCACTTTGGGATGTATTAGTTGAGATGGGGCCACAAGGAGCTGAAAGAGATTGGAATTGGAATT
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Sequence 311521, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: WOMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR FILING DATE: 2005-11-03

PRIOR PILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105482.2

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

PRIOR PILING DATE: 2005-07-18

PRIOR PILING DATE: 2005-07-18

PRIOR PILING DATE: 2005-07-18
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99.0%; Pred. No. 1.5e-175;
tive 0; Mismatches 7;
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Best Local Similarity 99.09
Matches 668; Conservative
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US-11-266-748A-311521
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                                 2; Gaps
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Multigan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 58815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
                              Indels
99.7%; Pred. No. 3e-149;
tive 0; Mismatches 0;
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   Best Local Similarity 99.73
Matches 592, Conservative
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          495 ATGCCCCCATCTGCTCTGCCCTCTTGTTACAAGCCTCAAGTGCTCAATGGTGTGAGAAGC 436
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f TYPE: DNA
c ORGANISM: Homo Sapiens
US-11-266-748A-99554

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                                                                                                                                                                                                                3194 ATTCAGAAGGTTTGTAACAAG-AAACTATGGGAAAGATACACTCACCGG-AGAAAGAAG 3251
                                                                                                                                                                                                                                                                                    TITCTGAAGAAAACCACAACCATGCCAATGAACGAATGCTATTTCATGGGTCTCCTTTTG 3311
                                                                                                                                                                                                                                                                                                                                                         TGAATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTG 3371
                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGC 3491
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APPLICANT: MAILIGAN, RATI
APPLICANT: MAILIGAN, RATI
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
                                                                                                                                           Query Match 15.0%; Score 570; DB 8; Length 594;
Best Local Similarity 99.7%; Pred. No. 3e-149;
Matches 592; Conservative 0; Mismatches 0; Indels
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APPLICANT: Harkin, Paul
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 152365
LENGTH: 594
                                                                     TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-152365
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Pred. No. 1.7e-139;
0; Mismatches 239;
PRIOR APPLICATION NUMBER: BP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFUMARE: Patentin version 3.3
LENGTH: 929
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Best Local Similarity 74.0%;
Matches 679; Conservative
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; ORGANISM: Homo Sapiens
US-11-266-748A-189602
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3435 GAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGCTGC 3494
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                                                            301 ATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAATGGCCTAGCATTAG 360
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                                                                                                                                                                                                                                              3675 TTATGAGGCCTGAAGGTATGGTCGATGGATAAATAGTTATTTTAAGAAACTAATTCCACT
                                                                                                                                                                                                                                                                              421 TTATGAGGCCTGAAGGTATGGTCGATGGATAAATAGCTATTTTAAGAAACTAATTCCACT
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                       3555 ATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCCAGTGAAATGGCCTAGCATTAG
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Sequence 217436, Application US/11266748A

Publication No. US208060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Rarlick
APPLICANT: Mulligan, Rarlick
APPLICANT: Mulligan, Rarlick
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A
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PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
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US-11-266-748A-217436
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2468 AAGGGACGAACACACTTTGTTTGTTGCTAGCCCATGGAGCTGACCCGACTCTTAAA 2527
                                                                                                              AATCAGGAAGGACAAACACCTTTAGATTTAGTTTCAGCGGATGATGTCAGCGCTCTTCTG 2587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGCTGC 3494
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                             AACCAGAAGGCCAGACGCCTCTGGATCTGGCAACAGCTGACGATATCAGAGCTTTGCTG 911
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APPLICANT: Hartin, Faul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE PRILING VARIEND NOS: 483996
SOFTWARE PRILING VARIEND NOS: 483996
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55144, Application US/11266748A, Publication No. US20060134663A1, GENERAL INFORMATION:
                                                                                                                                                                                                                      2588 ACAGCAGCCATGCCCCA 2605
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US-11-266-748A-55144
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Sequence 244089, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION: APPLICANT: Harkin, Paul
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SOFTWARE: PatentIn version 3.3
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ORGANISM: Homo Sapiens
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US-11-266-748A-165504/C

Sequence 165564, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: HORMATION:

APPLICANT: Johnston, Patrick

APPLICANT: Milligan, Karl

TITLE OF INVENTION: Methods of Using the Same
FILE REPERBENCE: 55815-0102 (319189)

CURRENT FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PLING DATE: 2004-11-03

PRIOR FILING DATE: 2005-01-18

PRIOR PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR PRIOR PRIOR VERGIN NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

PRIOR PRIOR PRIOR PRIOR VERGIN NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

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| LOCATION: (220)..(228)
| OTHER INFORMATION: n is a, c, g, or
US-11-266-748A-165504
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ORGANISM: Homo Sapiens
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                                                                                                                 526 GAGACATTGAAGGGGGTCAGTCTACACCCCTTCATTTTGCAGCTGGGTATAACAGAGTGT
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APPLICANT: MULIGAN, KAI
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2006-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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Query Match 13.3%; Score 503.2; DB 8; Best Local Similarity 76.2%; Pred. No. 2.3e-130; Matches 619; Conservative 0; Mismatches 193;
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-116071
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  Length 668;
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Willigan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: MUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: BP 04105499)
CURRENT APPLICATION NUMBER: EP 04105492
PRIOR APPLICATION NUMBER: EP 041054926
PRIOR PELING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PRING DATE: 2004-11-03
                                               13; Indels
Score 515.6; DB 8;
Pred. No. 5.9e-134;
0; Mismatches 13;
Query Match
Best Local Similarity 97.6%;
Matches 518; Conservative
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US-11-266-748A-116071
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2005-01-18

PRIOR PILING DATE: 2005-01-18

PRIOR PILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PACENTIN Version 3.3

SEQ ID NO 158235

LENGTH. 1000
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ORGANISM: Homo Sapiens
US-11-266-748A-158235
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Matches 619
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3478 TIGCCACAGGCAGCIGCICITITIGCCGGGTAACCTIGGGAAAGICTITICCTGCAGTITICAG 3537
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                                                                                                                                                            3598 AAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCCTGAGTA
                                                                              3538 TGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGT
                                                                                                                338 caccardaaaarddcccacdcdccrccadaccacrcadrcarrdgradaccaadcar
                                      398 ATGTCACAGACAAATGCTCTTCTGTAGAGTGACCCTTGGGAAATCCTTTCTGCAGTTAG
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Search completed: December 18, 2006, 19:31:47 Job time : 759.113 gecs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model
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December 18, 2006, 13:00:26; Search time 655.632 Seconds (without alignments) 10890.483 Million cell updates/sec Run on:

US-10-616-101-2 3816 Title: Perfect score:

Sequence:

IDENTITY NUC Scoring table: 1403666 segs, 935554401 residues Searched:

Gapop 10.0 , Gapext 1.0

2807332 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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9: /BMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_SIDS3.*
10: /BMC_Celerra_SIDS3/ptodata/2/ina/Packfiles1.seq:* Issued Patents NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

*	Description	Sequence 2, Appli	Sequence 2, Appli	'n	11,	556,	3, Aj	4	Sequence 1, Appli	ij	Sequence 1, Appli	'n	4	Sequence 1, Appli	'n	7	Sequence 7, Appli	Sequence 7, Appli	Sequence 9, Appli	6	40	Sequence 10, Appl		136
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SUMMARIES	, di	US-09-696-668-2	US-09-843-159B-2	US-09-972-115A-5	US-09-849-602-11	US-09-799-451-556	US-09-350-982C-3	US-09-350-982C-4	US-09-696-668-1	US-09-843-159B-1	US-09-427-154-1	US-09-972-115A-3	US-09-972-115A-1	US-09-196-387-1	US-09-841-835-1	US-09-972-115A-7	US-09-196-387-7	US-09-841-835-7	US-09-196-387-9	US-09-841-835-9	US-09-964-899-40	US-09-972-115A-10	US-09-972-115A-9	US-09-270-767-13625
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* 6	Match	100.0	100.0	99.4	99.3	98.8	94.2	. 91.4	88.9	88.9	88.8	87.6	79.6	49.4	49.4	49.4	39.9	39.9	35.9	35.9	31.3	13.6	10.0	6.5
	Score	3816	3816	3791.4	3788.4	3770.8	3594.8	3488.8	3393.4	3393.4	3387.6	3341	3039	1885	1885	1885	1521.2	1521.2	1369.4	1369.4	1192.6	518.4	.380.4	249.4
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Sequence 12, Appl	Sequence 12, Appl	Sequence 30, Appl	Sequence 1107, Ap	Sequence 35, Appl	Sequence 36, Appl	Sequence 35, Appl	Sequence 36, Appl	Sequence 35, Appl	Sequence 36, Appl	35,	Sequence 36, Appl	Sequence 32, Appl	Sequence 34, Appl			32,		Sequence 32, Appl	Sequence 34, Appl	Sequence 1788, Ap	Sequence 1789, Ap
US-09-196-387-12	US-09-841-835-12	US-09-220-132-30	US-09-949-016-1107	US-09-031-485-35	US-09-031-485-36	US-08-847-429A-35	US-08-847-429A-36	US-09-065-474-35	US-09-065-474-36	US-09-557-034-35	US-09-557-034-36	US-09-031-485-32	US-09-031-485-34	US-08-847-429A-32	US-08-847-429A-34	US-09-065-474-32	US-09-065-474-34	US-09-557-034-32	US-09-557-034-34	US-09-949-016-1788	US-09-949-016-1789
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121.2	121.2	97.4	97.4	93	66	93	93	93	93	93	93	93	93	93	93	93	93	93	93	8.06	8.06
24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	MBTT						
### SECTOR SECTOR SECTION 10.09696668 ### SERIOR NO. 6617102 ### SERIOR NO. 6617103 ### SERIOR NO. 6617103 ### SERIOR C. Chan, Eva APPLICANT: Luo, Ying ### SPELICANT: Luo, Ying ### SPELICANT: Luo, Ying ### SPELICANT: Huang, Betty ### SERIOR C. Chan, Eva APPLICANT: NUNCENTION: TANKTRASE H, COMPOSITIONS INVOLVED IN THE SPELICANT: APPLICANTON UNDERS: US 09/427,154 ### PRIOR APPLICANTON UNDERS: US 09/427,154 ### RIOR APPLICANTON UNDERS: US 09/427,154 ### CCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	AND	0;	09	120	180	240	300
SULT 1 -09-696-66809-696-6683equence 2, -3exera 1 No. 6	ahr a			GAGCCAAGCGGCCCGGG 	GGGCCGGGGCTCCTGC 		
SULT 1 -09-696-66809-696-6683equence 2, -3exera 1 No. 6	OSITIONS INVOLVED ,668 54	3816; DB 3; No. 0; natches 0;	scceegegcaggagg 	BATCCGGTGACAGCAGG 	cresecerecraserias 	stegegegeceagat 	agcgccgcggccgagg
SULT 1 -09-696-66809-696-6683equence 2, -3exera 1 No. 6	n US/09696668 tty a, Valeria ANKYRASE H, COMP- 22-17RMS/DHR UMBER: US/09/696 2002-07-23 2002-07-23 99-10-25 11 rsion 3.1	.08; Sc .08; Pr		CCATGGGACTGCGCGG 	GTCTTCTCCGGGGGGC 	gacgerarracrager 	GGGAGCGGCCTGCGCG
th the th	Applicatio 6617102 ORMATION: Luo, Ying Chan, Eva Xu, Xiang Huang, Be OBSOVSKAY NVENTION: ENCE: A-682 PLICATION NV NG DATE: 19 SEQ ID NOS: PACETION NV NG DATE: 19 SEQ ID NOS:	널					
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Sequence 2. Application US/09843159B

| Sequence 2. Application US/09843159B
| Patent No. 6887675
| GENERAL INFORMATION:
| APPLICANT: Chan, Evan
| APPLICANT: Chan, Evan
| APPLICANT: Chan, Evan
| APPLICANT: Chan, Evan
| APPLICANT: Muang, Betty
| TILE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods of TILE REFERENCE: A-68292-2/RMS/DHR
| CURRENT APPLICATION NUMBER: US/09/843,159B
| CURRENT FILING DATE: 2000-10-25
| PRIOR PILING DATE: 2000-10-25
| PRIOR PPLICATION NUMBER: US 09/427,154
| PRIOR PLING DATE: 1999-10-25
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: PatentIn version 3.1
| SOFTWARE: PatentIn version 3.1
| SOFTWARE: PatentIn version 3.1
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vative 0; Mismatches
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Query Match
Best Local Similarity 99.8
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CTHER INFORMATION:
US-09-972-115A-5
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US-09-972-115A-5
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APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/129,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
                                                                                                                                                                 99.4%; Score 3791.4; 99.8%; Pred. No. 0;
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3720 AGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATG 3779
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Sequence 11, Application US/09849602

Patent No. 6794501

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew J.

APPLICANT: Old, Lloyd J.

APPLICANT: Stockert, Elisabeth

APPLICANT: Chen, Yao-Tseng

TITLE OF INVENTION: Colon Cancer Antigen Panel

FILE REFERENCE: L0461/7105 (DRV)

CURRENT APPLICATION NUMBER: US/09/849,602

CURRENT PILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.0

LENGTH: 6018
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Matches 3803; Conservative
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CORGANISM: Homo sapien
US-09-849-602-11
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APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
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APPLICANT: Wang, Youqhong
APPLICANT: Wang, Youghong
APPLICANT: Wang, Wonghong
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APPLICANT: Wang, Wonghong
APPLICANT: Wang, Sunwell
APPLICANT: Wang, Sun
                                                                                                                Sequence 556, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                   2760 GTTTTTCAGAACTGTCTTCAGTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTTTGG 2819
                                                                                                                                                                              AGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCCAATTCGTAAGGAATCTTGGAC 2883
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120 GCAGGTTTTGGGCGGAAAGACGTAGATATTTGCTTCAGAATGGTGCAAATGTCCAA	CTCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGTGTG	780 8 808 A 840 G A 868 D G	900 ATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCGTGCTAAAGATAAAGGTGATCTG	988 GIACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTGAACTTTTGGTCAAG 1020 CATGGTGCTGTGAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCGCCT 1048 CATGGTGCCTGTGTAAATGCAATGGACTTGTGCCAATTCACTCCTCTTCATGAGGCAGCT 1080 TCTAAGAACAGGGTTGAAGTATCTCTTCTTTATGGTGCAACGCTGTGTGTG	1108 ICTARGARICAGASTICARAGIRICICITICICITIAGGIRGIGAGACCICARCACIG 1140 CTCARTGCCACATAAAAGTGCTATAGACTTGGCTCCCACCACCAGTTAAAAGAAAG	TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGTTG GAATCAAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACAC GAATCAAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACAC GAATCAAAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACAC CAGCATTGCATT	1348 ACAGCATTGCATTGTGCTGCTGCTATATCCCATATGCATATGTGAACTG 1407 1380 TTGCTAAGAAAGGAGCAAACATCAATGAAAGACTAAAGAATTCTTGACTCCTCTGCAC 1439

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CATAATGCATGCTCTTTTGGTCATGCTGAAGTAGTCAATCTCCTTTTGCGACATGGTGCA 367
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                                            Query Match
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3593; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: PCR Primers
NAME/KEY: misc_feature
LOCATION: (1124)
OTHER INFORMATION: n is any nucleic acid
NAME/KEY: misc_feature
LOCATION: (2672)
OTHER INFORMATION: n is any nucleic acid
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                           TTGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAAATTGTAAGGAATCTT
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Sequence 3, Application US/09350982C

Sequence 3, Application US/09350982C

Patent No. 6455290

GENERAL INFORMATION:
APPLICANT: Toma. Salvatore
APPLICANT: Toma. Salvatore
APPLICANT: Toma. Salvatore
TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Relat
TITLE OF INVENTION: Same
FILE REPERENCE: PHRM-0043
CURRENT APPLICATION NUMBER: US/09/350,982C
CURRENT APPLICATION NUMBER: US/09/350,982C
NUMBER OF SEQ ID NOS: 10
NUMBER OF SEQ ID NOS: 10 ö 127 389 449 247 509 187 307 67 330 GACGTGGAACGAGTCAAGAGGCTGGTGACGCCTGAGAAGGTGAACAGCCGCGACACGGCG TATTTGCTTCAGAATGGTGCAAGGCCGCGAGGTGATGGGGGGCCTTATTCCTCTT 3748 GGATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATAAGCAGCAGT 8 GCGCCGCCAGGATCATCATCTCGCGCTCGCCCCTGCGCCGGCGGAGCGGCCTGCCCCGCGGGC 68 GCCGCGGCCGAGGCCGTGGAGCCGGCCCGAGAGCTGTTCGAGGCGTGCCGCAAACGG 390 GGCAGGAAATCCACCCCGCTGCACTTCGCCGCAGGTTTTGGGCGGAAAGACGTAGTTGAA 188 GGCAGGAATCCACCCCGCTGCACCTCGCCGCAGGTTTTGGGCGGAAAGACGTAGTTGAA GGATAAATAGTTATTTTAAGAAACTAAATTCCACTGAACCTAAAATCATCAAAGCAGCAGT Gaps .. 0 DB 3; Length 4512; 5; Indels

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1770 AGTGTCAACTGCAGAGACATTGAAGGGCGTCAGTCTACACCACTTCATTTGCAGCTGGG 1829	1950 GAACTTCTTGTTAAACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCT 2009	2130 GATACAGATATTCAAGATCTGCTTAGGGGAGATGCTGCTAGATGCTGCCAAGAAG 2189	GAGTATTTGTTACAACAC GAGTATTTGTTACAACAC TTACATAATGCAGCATCT 	B GCATGITCAATGCCAACGAATGGGCTTTTCAACCTTTGCAACGAAGCAGCCCAAAAAAAA	GCAGCCATGCCCCATCTGCTCTTCTTCAGGTCCTCAGGTCCTCATGGTGG 246 AGAAGCCCATGCCCCTCTGCTCTCTTCAGGTCCTCAGGTCCTCATGGTGG 246 AGAAGCCCAGGAGCCACTGCAGATGCTCTCTTCAGGTCCATCTAGCCCATCAGGTGTT 272 AGAAGCCCAGGAGCCACTGCAGATGCTCTCTTCTTCAGGTCCATCAGCCCATCAGGCCTT 252 TCTGCAGCCAGCAGTCTTAACAACTTATCTGGAGATTTTTCAGAACTGTCTTCAGTAGTT 278 TCTGCAGCCAGCAGTCTTGACAACTTATCTGGAGATTTTTCAGAACTGTCTTCAGTAGTT 258 AGTTCAAGTGGAACAGGAGGTGCTTCCAGTTTTTGAGAAAAGGAGGTTCCAGGAGTAGAT 284 AGTTCAAGTGGAACAGGAGGTGCTTCCAGTTTTTGAGAAAAAGGAGGTTCCAGGAGTAGAT 284 AGTTCAAGTGGAACAGAGGGTGCTTCCAGTTTTGGAGAAAAAGGAGGTTCCAGGAGTAGAT 284
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AAGATTGATGTTTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACA GATGGAAGGACAGCATTGCTGTTACAGCATCCATCTGCCAAAGCAGTGCTTACTGGTGAA GATGGAAGGACGCATTGCATT	CTACTCACACCATTAAATGTCAACTGCCACGCAAGTGATGGCAGAAAGTCAACTCCATTA CATTTGGCAGCAGGATATAACAGGTAAAGATTGTACAGCTGTTACTGCAACTCCAACTCCATTA CATTTGGCAGCAGGATATAACAGGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCT GATGTCCATGCTAAAAAAAAAA	1050 TGGCAATTGAACTTTTTGGTCAAGCATGGTGTGTGTAAATGCAATGGAATGGAATTGGTGTGTGT	968 TTGGCTCCCACACACATTAAAAGAAAGATTACCATATTAAAGGCCACTCGTTG 1027 1230 CTGCAAGCTGCACGAGAAGCTAATTACTCGAAAACATCACACACA		1530 TCTCTACACAGAGCTGCATATTGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCTAT 1589 1328 TCTCTACACAGAGCTGCATATTGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCTAT 1387 1590 GGGTGTGATCCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAA 1449 1388 GGGTGTGATCCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAA 1447 1650 AATGTACAGCAACTCCTCCAAGAGGGTATCTCATTAGGTAATTCAGAGGCAGACAGA

Sequence 4, Application US/09350982C Patent No. 6455290

US-09-350-982C-4

APPLICANT: Berchelsen, Jens
APPLICANT: Toma, Salvatore
APPLICANT: Toma, Salvatore
APPLICANT: Toma, Salvatore
APPLICANT: Toma, Salvatore
TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Relat
TITLE OF INVENTION: Same
FILE REPERBNES: PHRM-0043
CURRENT FILING.DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 449 ö 344 120 180 300 420 284 404 464 524 584 360 644 704 TIGGATITIAGCAGAICCAICTIGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGAIGAA 764 CTCTTAGAAAGTGCCAGGAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTA 824 9 405 CCGCTGCACTTCGCCGCAGGTTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAT

181 CCGCTGCACCTCGCCGCAGGTTTTGGGCGGAAAGACGTAGTTGATTTTGCTTCAGAAT 225 ATGTCGGGTCGCCGCTGCGCCGGCGGGGGGCGCCTGCGCGCGAGCGCCGGCGGCCGAGGCC 1 ATGTCGGGTCGCCGCTGCCCGCGGGGGAGCGCCTGCGCGAGCGCCCGCGGCCCGAGGCC 121 AAGAGGCTGGTGACGCCTGAGAAGGTGAACAGCCGCGACACGGCGGGCAGGAAATCCACC 301 TTTGGTCAAGCTGAAGTAGTCAATCTCCTTTTGCGACATGCAGACCCCAATGCTCGA 345 AAGAGGCTGGTGACGCCTGAGAAGGTGAACAGCCGCGACACGGCGGGCAGGAAATCCACC TTTGGTCATGCTGAAGTAGTCAATCTCCTTTTGCGACATGGTGCAGACCCCCAATGCTCGA ATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCA 585 GATAATTGGAATTATACTCCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGC Gaps ; 0 DB 3; Length 3498; 5; Indels 91.4%; Score 3488.8; 99.7%; Pred. No. 0; tive 6; Mismatches NAME, KEY: CDS
LOCATION: (1).. (3498)
NAME, KEY: CDS
LOCATION: (1).. (3498)
NAME, KEY: misc feature
OTHER INFORMATION: Xaa is any amino acid
NAME, KEY: misc feature
LOCATION: (1102).. (1102)
OTHER INFORMATION: n is any nucleic acid
NAME, KEY: misc feature
LOCATION: (2650).. (2650)
OTHER INFORMATION: n is any nucleic acid
OTHER INFORMATION: n is any nucleic acid Query Match Best Local Similarity 99.7° Matches 3487; Conservative ORGANISM: Artificial LENGTH: 3498 465 525 645 705 481 765 541 TYPE: DNA FEATURE: g 셤 셤 g 용 셤 ð 셤 ઠ ઠે 셤 ઠે ò 셤 Š ò ò ð ઠે

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825 AATGTCAACTGCCACGCAAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGA 884	0y 11	GATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACT 	GAACTITIGGCAAGGATGGTGCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCT	1124	0y 1125 GCAGACCCAACACTGCTCAATTGTCACAATAAAGTGCTATAGACTTGGCTCCCACCACA 1184	CACGA 1244	OY 1245 GAAGCTGATGTTACTCGAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCAT 1304 1021 GAAGCTGATGTTACTCGAATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCAT 1080	097 1305 CCTCAAACACATGAAACAGCATTGCATTGTGCTGCTGCATCTCCAAAAGAAAG	OY 1365 CARATATGTGAACTGTTGCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTC 1424	rccrc 1484	3AGCT 1544 3AGCT 1320	1545 GCATATTGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAAC 1604	ATTATATCCCTTCAGGGCTTTACTGCTTTACAGAAATGGAAATGAAAATGTACAGCAACTC 1664	CTGCA 1724	3CAGA 1784 3CAGA 1560	GACATTGAAGGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCC	GTGGTGGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCTT	1621 GTGGTGGAATATCTGCTACAGCATGGAGCTGATGTGCTAAAGATAAAGRRGSCCTT 1680 Qy

	Query Match 88.9%; Score 3393.4; DB 3; Length 3797; Best Local Similarity 99.9%; Pred. No. 0; Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	OY 422 AGGITITGGGCGGAAAGACGTAGATATATTTGCTTCAGAATGGGCAAATGTCCAAGC 481	Qy 482 ACGTGATGATGGGGGCCTTATTCCTCTTCATAATGCATGC	OY 542 AGTCAATCTCCTTTTGCGACATGGTGCAGACCCCCAATGCTCGAGATAATTGGAATTATAC 601	OY 602 TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGCA 661	OY 662 TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC 721	OY 722 ATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG 781 	OY 782 GAGTGGCAATGAAGAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCAGGC 841	OY 842 AAGTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGAT 901.	OY 902 TGTACAGCTGTTACTGCAACATGGGGCTGATGTCCATGGTAAAGATAAAGGTGATCTGGT 961	OY 962 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGTGATCTATTGGTCAAGCA 1021	OY 1022 TGGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTC 1081	QY 1082 TAAGAACAGGGTTGAAGTATGTTCTCTTCTTCTTAAGTTATGGTGCAGACCCAACACTGCT 1141	QY 1142 CAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACACA	OY 1202 AGCATATGAATTTAAAGGCCACTGCTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCG 1261	Qy 1262 AATCAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAAC 1321 	OY 1322 AGCATTGCATTGCTGCTGCATCTCCATATCCCAAAGAAAG	OY 1382 GCTAAGAAAGGGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACGT 1441
aactaattaaaggagtcgagagacttatctccggacaagag	OY 3045 AACCCATATTAACTTTGAACACCTCTGGTAGAACAATTCTTATAGATCTGTCTCT 3104	OY 3105 GATGATBAAGAGTTTCAGTCTGTGGAGGAAGAGTGCAAAGTACAGTTCGAGAGCACAGA 3164 DD 2881 GATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAAGTACAGTTCGAGAGCACAGA 2940	OY 3165 GANGGAGGTCATCCAGGTGGAATCTTCAACAGATACAATATTCTCAGATTCAGAAGGTT 3224	OY 3225 TGTAACAAGAAACTATGGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAAAC 3284 	OY 3285 CACAACCAAGCCAATGAACGAATGCTATTTCATGGGTCTCCTTTTGTGAATGCAATTATC 3344	dy 3345 CACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTAT 3404 Db 3121 CACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTAT 3180	Qy 3405 TTTGCTGAAAACTCTTCCAAAAGCAATCAATATGTATATGGAATTGGAGGAGGTACTGGG 3464	Oy 3465 TGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGG 3524 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy · 3525 GTAACCTTGGGAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCA 3584	OY 3585 GGTCATCACTCACTCGCTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATTT 3644	OY 3645 ATTTACAGAGAGAAACAGGCTTATCCTGAGTATTTAATTACTTAC	Qy 3705 GAAGGTATGGTCGATGGA 3722 Db 3481 GAAGGTATGGTCGATGGA 3498	RESULT 8 US-09-696-668-1	; Sequence 1, Application US/0969668 ; Patent No. 6617102 ; GENERAL INFORMATION: ; APPLICANT: Luo, Ying	-	111LE OF INVENTION: TANKKRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS FILE REPERENCE: A-68292-1/RMS/DHR CYCLE US/09/696,668 CURRENT APPLICATION NUMBER: US/09/696,668 CURRENT FILING DATE: 2002-07-23	; PRIOR APPLICATION NUMBER: US 09/427,154 ; PRIOR FILING DATE: 1999-10-25 ; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: Patentin version 3.1	; SEQ ID NO 1 ; LENGTH: 3197 ; TYPE: DNA ; ORGANISM: Homo sapiens

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3583 TGGTAGGCCCAGTGTAAATGGCCTAGCATAATGTTATTTACAGAGGAGAACA 3642	3662 GGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGG 3721 	ataaatagttatttaagaaactaattccactgaac 	3782 CCTCTACGTTTTACTCCTGAAAAAAA 3816 	SULT 9 :-09-843-159B-1 sequence 1, Application US/09843159B	GENERAL INFORMATION APPLICANT: Luo, Yin APPLICANT: Chan, Evan	APPLICANT: Au. Araug APPLICANT: Huang, Betty TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods FILE REPRENCE: A-68929-Z/RMS/DHR TIDDERM: ADDITANTON NUMBED: 116/06/04/3-1600	CURRENT FILING DATE: 2001-04-25 PRIOR APPLICATION NUMBER: US 09/696,668 PRIOR FILING DATE: 2000-10-25 PRIOR FILING DATE: 2000-01-25	FRIOR FILING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 17 SOTTWARE: Patentin version 3.1	LENGTH: 3797 TYPE: DNA ORGANISM: Homo sapiens	Query Match 88.9%; Score 3393.4; DB 3; Length 3797; Best Local Similarity 99.9%; No. 0; Marche 1394 Concaverite 0. Mismarches 1. Indole 0. Gane 0.	GENERAL SECTION OF THE SECTION OF TH				TGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCC			/83 GAGIGGCAAIGGAAAAAAAIGGIGICIACICACCAIIAAAIGICAACIGCCACGC 822

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2983 AATTANAGGAGTCGAGAGATTATCTCCGGACACAGGTCTTAACCCATATTAACTTT 3042 3062 GAACACCTTGGTAGTGGAACATTCTTATAGATTCTGTCCCGAGAGATGGATG	RESULT 10 US-09-427-154-1 Sequence 1, Application US/09427154 Sequence 1, Application US/09427154 Patent No. 6589725 GENERAL INPORMATION: APPLICANT: Luo, Ying APPLICANT: Luo, Ying APPLICANT: Xu, Xiang APPLICANT: Xu, Xiang APPLICANT: Nu Xiang APPLICANT: 1
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1993 TGTRGCTGATTATGGAACTTGCTGATGGAGGAGGAAAGGAA	2762 GAGTITITCAGAACTGTCTTCAGTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTTT 2821 2743 GAGTITTTCAGAACTGTCTTCAGTAGTTCAGTGGAACAGAGGGTGCTTCCAGTTT 2802 2822 GGAGAAAAGGGTTCCAGGAGTAGTTTAGCTTAACTGAACTGATTCGTAAGGAATTTTGGGAACAGAACTGTTTGGGAACTGATTTTAGCATAACTGAATTCGTAAGGAATTTTGGGAACATAACTCATTGGAATTTTTAGCATAACTCAATTCGTAAGGAATTGTTGG 2861 2803 GGGAAAAAAGGAGTTCCAGGAGTATTTTAGCATAACTCAATTCGTAAGGAATTTGTTGG 2862 2804 ACTTGAGCACCTAATGGATATTTTGAGAACAGAACAGATCACTTTGGATGTTTAGTTGA 2941 2803 ACTTGAGCACCTAATGGATATTTTTAGGAACAGAACACACTTTGGATGTTTAGTTGA 2922 2942 GATGGGGCACAAGGAGTGATATTTTTAGGAACAACACATTTTTAGATGATTGAT

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Sequence 3, Application US/09972115A
Patent No. 6599728
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                                                                                                        GCGGATGATGTCAGCGCTCTTCTGACAGCCAGCCATGCCCCCATCTGCTCTGCTCTTGT
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NAME/KEY: CDS
LOCATION: (1). (3801)
OTHER INPORMATION:
NAME/KEY: Misc_feature
LOCATION: (1). (1)
OTHER INPORMATION: in to provide alignment.
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (125). (125)
OTHER INPORMATION: in to provide alignment.
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (239). (1230)
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (320)
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: sequences not determined at this position. Unknown residue put
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: sequences not determined at this position. Unknown residue put
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: Lot provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: Lot provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
OTHER INPORMATION: Lot provide alignment.
NAME/KEY: misc_feature
LOCATION: (310). (310)
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NAME/KEY: misc_feature
LOCATION: (415). (415)
OTHER INPORMATION: equences not determined at this position. Unknown residue put
OTHER INPORMATION: Lot provide alignment.
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3603 GGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAG
                                                                                                                                                                                                                                                 3241 GCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATGGA
                                                                                                                                                                                                                                                                                                                               3723 TAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAGCAGCAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Geron Corporation.
APPLICANT: Gragg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REPERBNCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 4297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CICTACGITITACICCITIGCIGAAAAAAAAA 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3361 CTCTACGTTTTACTCCTTTGCTGAAAAAAAAA 3394
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; LOCATION: (2180)(2180) ; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put ; OTHER INFORMATION: in to provide alignment. ; NAME/KEY: misc feature	ION: (2205)(2205) INFORMATION: Sequences not determined at this position . Unknown residue INFORMATION: in to provide alignment. KEY: misc feature ION: (2221)(2221)	determined at this position alignment.	INFORMATION: Sequences not determined at this position . Unknown residue INFORMATION: in to provide alignment. EXY: misc feature ION: (2316)(2316) INFORMATION: Sequences not determined at this position . Unknown residue	ORMATION: in to provide alignment. misc feature (2359)(2674). ORMATION: Sequences not determined at this position . Unknown residue ORMATION: in to provide alignment.	ure 2977) Sequences not in to provide	i OTHER INFORMATION: sequences not determined at this position . Unknown residue put ; OTHER INFORMATION: in to provide alignment. US-09-972-115A-3	Query Match 87.6%; Score 3341; DB 3; Length 4297; Best Local Similarity 89.0%; Pred. No. 0; Matches 3400; Conservative 8; Mismatches 402; Indels 12; Gaps 2;	Qy 1 CGCGCTGCTCCGCCGCGGGGGCAGGGGGGGGGGGGGGGG	OY 61 TGGGCGCGCCCATGGGACTGCGCCGGATCCGGTGACGGGGGCCAGCGGGCCCGGG 120	Oy 121 CCCTGAGCGCGTCTTCTCCGGGGGCCCTCCTGCTGCGGGGCCGGGGCTCCTGC 180	AY 181 TCCGGTTGCTGGCGCTGTTGCTGGCGGCGGCGGGGCCAGGATCATGTCGGGTCGCCGCT 240	QY 241 GCGCCGGCGGGGGGGGCCTGCGCGCCGCCGCCGGCCGGGCCGGCCCGCCC 300 Db 314 GCGCCGGCGGGGGGANCGGCCTGCGCGANCGCCGGANCGCCGGANCGCCCCCCCC	OY 301 GACAGCTGTTCGAGGCGTGCCGCACGGGACGTGGAACGAGTCAAGAGGCTGGTGACGC 360	Oy 361 CTGAGAAGGTGAACAGCGGGGACACGGGAGGAAATCCACCCGGTGCACTTGGCCG 420	OY 421 CAGGITITIGGGCGGAAAGACGTAGITIGATATTIGCITCAGAAIGGIGCAAAIGTCCAAG 480	Qy 481 CACGTGATGATGGGGGCCTTATTCCTCTTCATAATGCATGC
Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put
NAME/KEY: misc feature LOCATION: (432)(432) OTHER INFORMATION: Sequences not determined at this position . I	nences not determined at this position . to provide alignment.	ences not determined at this position . o provide alignment.	ences not determined at this position . o provide alignment.	determined at this position . alignment. determined at this position .	<pre>provide alignment. inces not determined at this position . provide alignment.</pre>	Lences not determined at this position .	<pre>lences not determined at this position . lence an incomment.</pre>	<pre>lences not determined at this position . co provide alignment.</pre>	Lences not determined at this position .	nences not determined at this position .	uences not determined at this position . to provide alignment.	uences not determined at this position . to provide alignment.	NAME/RAT: MISC. Teature LOCATION: (711)(713) OTHER INFORMATION: Sequences not determined at this position . U OTHER INFORMATION: in to provide alignment.	 section of determined at this position . provide alignment. 	Leacure 5)(2000) ION: Sequences not determined at this position . GON: in to provide allgnment.	s) uences not determined at this position . to provide alignment.

us-10-616-101-2.rni

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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                TAATTAAAGGAGTCGAGAGACTTATCTCCGGACAAAGAGGTCTTAACCCATATTTAACTT 3060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3611 TGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCCAGGTCATC 3670
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2771 CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGCAGCAGCAGTCTTGACAACTTATCTG 2830
                                                                                                                               TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCTGTGGAGGAAGAGATGCAAAGTACAGTTCGAGAGACACAGAGAGATGGAGGTCATGCAG 3250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAAC-----A 3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3311 TTCGGCACGAGGAAGATACACTCACCGGAGAAAGAAGTTTCTGAAGAAAACCACAACC 3370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAACTCTTCCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAG 3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3491 AAAACTCTTCCAAAAGCAATCAATATGTATATGGAATTGGAGGAGGAGCTACTGGGTGTCCAG 3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATC 3591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGAGAACAGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTA 3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTCGATGGATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAA 3771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCAGTCACTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACA
                                                                                    2831 GGAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAACACCTCTGGTAGTGGAACAATTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTC
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NAME/KEY: misc. feature.

LOCATION: (724) .. (724)

OTHER INFORMATION: Sequences not determined at this position of THER INFORMATION: in to provide alignment.

LOCATION: (730) .. (730)
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OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
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NAME/KEY: misc. feature
LOCATION: (625)..(626)
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LOCATION: (1). [586)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
LOCATION: (596). (597)
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Sequence I. Application US/09972115A
Patent No. 6599728
GENERAL INFORMATION:
APPLICANT: Greeg Morin B.
APPLICANT: Greeg Morin B.
APPLICANT: Walter, Funk D.
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOCTWARE: PatentIn version 3.1
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LOCATION: (638)..(638)
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LOCATION: (791)..(791)
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LOCATION: (1)..(3999)
OTHER INFORMATION:
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	CAGCAGATATAACAGAGTAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTC	1187 ATGCTAAAGATAAAGTGATCGTACCATTACACAATGCCTGTTCTTATGGTCATTATG 1246	GTTATGGTGCAGACCAACACTGCTCAATTGTCACAATAAAGTGCTATAGACTTGGCTC 117 GTTATGGTGCAGACCCAACACTGCTCAATTGTCACAATAAAAGTGCTATAGACTTGGCTC 117 GTTATGGTGCAGACCCAACACTGCTCAATTGTCACAATAAAAGTGCTATAGACTTGGCTC 142 CCACACCACAGTTAAAAGAAAGATTAGCATATGAATTTAAAAGGCCACTCGTTGCTGCAGAG 123	CACAGE TAGARAGA TAGARAGA TAGARAT TAGARAGA TAGARAT TAGARAGA TAGARAT TAGARAGA TAGA T	AAAGAAAGCAAATATGTGAACTGTTGCTAAGAAAAGGAGCAAAAGAAAG	1477 TAGTGGTGARACATGARGGTRAATGCTCTGGATAATCTTGGTCAGACTTCTCTAC 1536	
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C1148) Sequences not determined at this position . Unknown residue put in to provide alignment. C177) Sequences not determined at this position . Unknown residue put in the provide alignment.	ces not determined at this position . Unknown residue put provide alignment.	ignment. itermined at this position . Unknown residue ignment.	provide alignment. ces not determined at this position . Unknown residue put provide alignment. ces not determined at this position . Unknown residue put	in to provide alignment. (1163) Sequences not determined at this position . Unknown residue put in to provide alignment. ture (13499) Sequences not determined at this position . Unknown residue put in to provide alignment.	Score 3039; DB 3; Length 4493; Pred. No. 0; 1; Mismatches 375; Indels 27; Gaps Indels 27; Gaps 39 Indels 27; Gaps 27; G	CAGGA 64 TTTGC 45 TTTGC 70 TAATG 51	TTCAAAATGGTGCAAATNTCCAANCACTTTATAATGGGGGCCTTATTCCTCTTCTCATAATG 766 CATGCTCTTTGGTCATGCTGAAGTAGTCAATCTCCTTTTGCGACATGGTGCAGACCCCA 576 CATGCTCTTTTGGTCATGCTAAAANTATCAATCTCCTTTTGCGACATGGTGCAGACCCCA 826 GTGCTCGAGATAATTGGAATTATACTCCTCTCCCTTTGCGACATCAAGGAAGATTG 636 ATGCTCGAGATAATTGGAATTATACTCCTCTCCCTGAAGCTGCAATTAAAGGAAAGATTG 636 ATGTTTGCATTGTGCTGTTACAGCATGGAGCTGAGCTACTCCGAAATTAAAGGAAAGATTG 886 ATGTTTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAA 946 GGACAGCATTGGCTGTTACAGCATCGCCAAAGCAGACCATCCGAAATACAGATGGAA 946 GGACAGCATTGGCTGTTACAGCATCTGCCCAAAGCAGTGCTTACTGGTGAATAAAGA 756 GGACAGCATTGGATTTAGCAGATCCATCTGCCCAAAGCAGTGCTTACTGGTGAATAAAGA 1006
AME/KEY: misc_feature ACATION: (2148)(2148) THER INFORMATION: Sequent THER INFORMATION: In to I AME/KEY: misc_feature ACATION: (2177)(2177) THER INFORMATION: Sequent	AME/KEY: misc feature ACCATION: (2382) THER INFORMATION: Sequences not de YTHER INFORMATION: In to provide al AME/KEY: misc feature (2398). (2398). THER INFORMATION: OF THE	VTHER INFORMATION, in to provide a TAMENTEY misc feature (AMENTAL) (246) (246) (246) (246) (248)	THER INFORMATION: In to provide the two control of two cont	THEK INFOKAMION: IN CO PIOVIGE MANAGEMENT (1163). (3163). (3163). (3163). (3163). (3163). (3163). (3163). (3163). (3163). (3163). (3199). (3188). (3199). (3188). (318	-1157 atch cal 8 3101		107 TTCAAAATGGTGCAA. 517 CATGCTCTTTTGGTC 767 CATGCTCTTTTGGTC 577 ATGCTCGAGATAATT 827 ATGCTCGAGATAATT 637 ATGTTTGCATTGTGC 637 ATGTTTGCATTGTGC 637 ATGTTTGCATTGTGC 647 GGACAGCATTGTGC 697 GGACAGCATTGTGT 747 GGACAGCATTGGATT 748 ATGTTTGCATTGTGC 749 ATGTTTGCATTGTGC 740 ATGTTTGCATTGTGC 740 ATGTTTGCATTGTGCT 741 ATGTTTGCATTGTGCT 741 ATGTTTGCATTGTGCT 741 ATGTTTGCATTGTGCT 741 ATGTTTGCATTGTGCT 741 ATGTTTGCATTGTGTT 741 ATGTTTGCATTGTGTT 741 ATGTTTGCATTGTGTT 741 ATGTTTGTGTT 741 ATGTTTGTT 741 ATGTTTT 741 ATGTTT 741 ATGTT

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1315	RESULT 13 US-09-196-387-1 ; Sequence 1, Application US/09196387 ; Patent No. 6277613 ; APPLICANT: de Lange, Titia ; APPLICANT: Smith, Susan ; TITLE OF INVENTION: OF USE THEREOF ; TITLE OF INVENTION: OF USE THEREOF
1837 GAGTOTTCOTOGTGAATATCTGCTACACATGGACTGATGCTGAAAGTAAAG 1897 GAGGCTTGTACCTTGCTAATATCTGCTACACATGGACTGATGATAAGTAAAG 1897 GAGGCTTGTACCTTTGCCAATACTTGCACATGATAAGTACTTTACACATTTACACTTTACACATTTCCTGCAAAATTTCCTGAAAATTTCCTGCTACACTTTACACATTTACACTTTTACACTTACACTTACACTTTACACTTTACACTTTACACTTTACACTTTACACTTTACACTTTACACTTTACACTTTACACTTTACACACTTACACTTACACTTACACTTACACACTTACACACTTACACACTTACACACTTAC	2791 GTTCAAGTGGAACAGAGGTGCTTCCAGTTTGGAGAAAAGGAGGTTCCAGGAGTAGATT 2850

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                   GCAGTGCTTACTGGTGAATATAAGAAGATGAACTCTTAGAAAGTGCCAGGAGTGGCAAT
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49.4%; Score 1885; DB 3; Length 4134;
Best Local Similarity 72.1%; Pred. No. 0;
Matches 2496; Conservative 0; Mismatches 940; Indels 27
                                                                                                                                       COMPUTER: PLORPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 260-1-230 CIP1
TELECONMUNICATION INFORMATION:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
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201-343-1684
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STRANDEDNESS: double
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3246 AAAGGAGTAGAAAGACTCTTAGGTGGACAACAAGGCACCAATCCTTATTTGACTTTTCAC
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO T
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
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ZIP: 07601
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US-09-841-835-1
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      MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING APPLICATION:
PRIOR APPLICATION NUMBER: 09/196,387
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JGAENT INFORMATION:
NAME: JGAENT NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDN
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; TYPE: DNA
; ORGANISM: Homo sapiens
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3246 AAAGGAGTAGAAAAGACTCTTAGGTGGACAACAAGAAGGACCAATCCTTATTTGACTTTTTCAC
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GENERAL INFORMATION:
APPLICANT Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Malter, Funk D.
APPLICANT: Mieczyslaw, Piaryszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR APPLICATION NUMBER: US 60/129,123
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 4134 ; Sequence 7, Application US/09972115A; Patent No. 6599728

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2607 AAGGGTG	2412 CTACTAA? 2667 TTATTGA?	2472 CACGAAGO 	2532 GACCCGAC 2787 GACCCCAC	2592 GTCAGCG(2847 ATCAGAGG	2652 CAAGTGCT 2907 CAGG	2712 TCTAGCCC 	2772 GAACTGTC 3006 GAGTTGG	2832GP 1 3066 GAAGGAGA	2886 GAGCACCT 3126 GAACACCT	2946 GGGCACAA 3186 GGTCATGA	3006 AAAGGAGT 3246 AAAGGAGT	3066 ACCTCTGG	3126 GTGGAGGP 3366 GTGGAAGP	3186 ATCTTCAP 3426 ATCTTCAP	3246 AGATACAC 3486 CGCTTCTQ	3306 ATGCTATT 3546 ATGTTGTT	3366 CATGCGTA 3606 CATGCATA	3426 AGCAATCA 3666 AGCAACCA

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3486 ICTIGITACATTIGCCACAGCAGCIGCICITITIGCCGGGTAACCTIGGGAAAGTCTITC 3545	CATGCTATATATATGCTCAGACAAATGCTCTTCTGTAGAGTGACCCTTGGGAAATCCTTT	3546 CIGCAGTICAGIGCAAIGAAAATGGCACATICCTCCTCCAGGTCATCACTCAGTCACTGGT 3605	CTGCAGTTTAGCACCATGAAAATGGCCCACGCGCTTCCAGGGCACCACTCAGTCATTGGT	3606 AGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCT 3665	AGACCGAGCGTCAATGGCGTGCCTGATATGCTGATATGTCATCTACAGAGGAGAACAGGCA	3666 TATCCTGAGTATTTAATTACCAGATTATGAGGCCTGAAG 3708	3906 TACCCAGAGTATCTTATCACTTACCAGATCATGAAGCCAGAAG 3948	
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Search completed: December 18, 2006, 16:38:05 Job time : 666.632 secs

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Adp77067 Tankyrase
Adh69415 Human tan
Adv85294 Human tan
Aac66825 Human tan
Aaf63952 Human tan
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Adr66604 Human pro
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ALIGNMENTS

RESULT 1

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Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation; cell cycle protein; cell cycle associated disorder; cancer; gene mapping; chromosome mapping; gene therapy; vaccine; ds.
                                                                                                                      Location/Qualifiers
2. 3726
4'teg= a /*teg= a //partial
fproduct= "TaHo2"
fnoctore= "Tankyrase homologue isotype 2; No start codon given"
                                                           Tankyrase homologue isotype 2 coding seguence.
       AAA91488 standard; DNA; 3816 BP
                                          (first entry)
                                                                                                                 Unidentified
                                          06-AUG-2001
                         AAA91488;
AAA91488
         11X88X1X8X3X1X6X8X1111111114X8X6X6X6X6X6X6X6X
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Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating

Huang

25-OCT-2000; 2000WO-US041528.

WO200130987-A2

03-MAY-2001.

99US-00427154

25-OCT-1999;

(RIGE-) RIGEL PHARM INC Luo Y, Chan E, Xu X, WPI; 2001-300503/31. P-PSDB; AAY97749. us-10-616-101-2.rng

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This sequence encodes the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-1 protein. The TaHo proteins are useful for inducing or preventing cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also cusful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vacine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with cuseful in screening assays or preventing cell cycle associated disorders such as cancer Claim 13; Fig 2; 63pp; English

Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

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ö 120 480 120 180 180 240 240 300 360 360 420 420 CAGGTTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAATGGTGCAAATGTCCAAG 480 540 540 TAGTCAATCTCCTTTTGCGACATGGTGCAGACCCCCAATGCTCGAGATAATTGGAATTATA 600 9 9 720 ececcedececeses de constantes 9 9 CGCGCTCCGCCCGCCGCGGGGCAGCCGGGGGGCAGGGAGCCCAGCGAGGGGCCCCC TGGGCGCGGCCCATGGGACTGCGCCGGATCCGGTGACAGCAGGGAGCCAAGCGAGCCGGG GAGACCTGTTCGAGGCGTGCCGCAACGGGACGTGGAACGAGTCAAGAGGCTGGTGACGC CTGAGAAGGTGAACAGCCGCGACACGCCGGCGGCAGGAATCCACCCCGCTGCACTTCGCCG CAGGTTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAATGGTGCAAATGCTCAAG TAGICAATCICCITITIGCGACATGGIGCAGACCCCAATGCICGAGATAATTGGAATTATA ATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATC CGCGCTGCTCCGCCCGCCGCGGGGCAGCCGGGGGCAGGGAGCCCAGCGAGGGGCGCGCG TGGGCGCGCCCATGGGACTGCGCCGGATCCGGTGACAGCAGGGAGCCAAGCGGCCCGGG CCCTGAGCGCGTCTTCTCCGGGGGGCCTCGCCCTCCTGCTCGCGGGGCCGGGGGCTCCTGC cecranacacacaretrerecadadacereacerecraereacadadacacacareerac GAGAGCTGTTCGAGGCGTGCCGCAACGGGACGTGGAACGAGTCAAGAGGCTGGTGACGC CTGAGAAGGTGAACAGCCGCGACACGCCGGCAGGAAATCCACCCCGCTGCACTTCGCCG CTCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGC ATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATC Gapa ö 100.0%; Score 3816; DB 4; Length 3816; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 3816; Conservative ч 61 121 181 181 241 241 361 121 541 501 561 Query Match Best Local S 121 301 301 361 421 181 481 541 601 561

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à	781	
Q Q	781	GGAGTGGCAATGAAAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACG 840
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q	841	CAAGIGATIGGCAGAAAGICAACICCATTACATTTGGCAGGATATAACAGAGTAAAAA 900
è 1	901	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGG 960 TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGTCAAGGTAAAGGTGATCTGG 960 TTGTACAACATAAAAGATAAAGGTGAACATGAAGATAAAAGATAAAAGATAAAAGATAAAAGAAAAAGAAAAAGAAAAAA
3 2	106	TECTATACATATACATACATACATACATACATAATAAAAAAA
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à	1021	AIGGIGCCIGIGIAAAIGCAAIGGACIIGIGGCAAIICACICCICIICAIGAGGCAGCII 1080
qq	1021	Argerecciercialarecaltegactrerescaltreactectertreaggedent 1080
à	1081	CTAAGAACAGGGTTGAAGTATGTTCTCTTTTAAGTTATGTGCAGACCCAACACTGC 1140
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ò	1141	TCAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCCACACCACAGTTAAAAGAAAG
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ò	1201	TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGTGCACGAGAAGCTGATGTTACTC 1260
Db	1201	radcarardaatrraaaddccacrccardcrccaagcrdcacaaadcrgargrracrc 1260
ò	1261	GAATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAA 1320
QQ	1261	GAATCAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACCACATGAAA 1320
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qq	1441	regerictergaraecteatrateatettetteraetreferererateraeaetrare
ò	1501	TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATC 1560
q	1501	TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATC 1560
λ	1561	TACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG 1620
QQ	1561	TACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG 1620
à	1621	GCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCT 1680
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ò	1741	AAACTGTAAAAAAACTGTACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGCGTC 1800
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10	ABO77067 ABO77067 ID ABO77067 XX XX XX DT 08-APR-2003 (first entry) XX XX DE Tankyrase H.isotype 2 TaHo-2 DNA from clone K23.
	GGAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAACGAACAAGAGGGTGCTTCCAGTT GGAGTTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAAGGGGAACAGAGGGTGCTTCCAGTT TGGAGAAAAGGGAGGTTCCAGGAGTAGTTTTAGCATAACTCAATTCGTAAGGAATCTTG TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG GACTTGAGCACCTAATGGATATTTGAGAGAACAGATCACTTTGGATGTATTAGTTG

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         Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2; TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour; cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of tumour cell. The methods are useful for screening for a bioactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or PARP (poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence encodes the tankyrase H isoform 2, TaHo-2, isolated from clone K23 which is described in the disclosure of the invention
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                                                                                                                                                            The invention relates to a method for screening a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21. The invention is useful in gene therapy. The method is useful for screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for preparing a composition for diagnosing or treating cancer. The present sequence is human tankyrase homologue isotype 2 (TaHo-2) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for diagnosing or treating cancer by combining a tankyrase H cell cycle protein, a candidate bioactive agent and p21.
                                                                                                     AGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATG
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bioactive agent screening; cancer; cytostatic; gene;
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The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (TaHo), comprising an amino acid sequence having 85% or more sequence identify to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (1) diagnosing cancer, which involves determining the activity of control with a control; (2) treating (M1) an individual mith a cell cycle control with a control; (2) treating (M1) an individual mith a cell cycle related disorder, which involves administering to the individual an control with a control; (3) a recombinant nucleic acid (II) encoding (II), comprising a nucleic acid that hybridizes under high stringent conditions to a sequence complementary to the 3797 base pair sequence of ADY97759 or the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or more sequence identity to ADY97759 or ADY97760; (4) an expression vector (III) comprising (II) operably linked to regulatory sequences recognized by a host cell (IV) transformed with the nucleic acid having 85% or comprising (II) or (III); (6) producing (I); (7) a polypeptide that comprising (II) or (III); (6) producing (I); (7) a polypeptide that confinition TaHo activity; (1) is useful for screening a bioactive agent capable of modulating (I); (1) as useful for treating endicing with the binding of (1), or screening for agent e.g. antisense collowate in the present sequence encodes the human tankyrase
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100.0%; Score 3816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3816; Conservative 0; Mismatches
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                                                                              Chan E, Xu X,
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(HUAN/) HUANG B.
(OSSO/) OSSOVSKAYA V.
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361 AGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCCTGAAGGTATGGTCGATG 3720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human SPANK cDNA. The SPANK protein comprises 3 domains: (a) a SAM (sterile alpha motif) domain; (b) a PARP (poly adenosine diphosphate-ribose polymerase) cardalytic domain; and (c) an ANK domain composed of ankyrin repeats. SPANK is a cytosolic protein which can poly(ADP-ribosyl) are itself. SPANK binds insulin-responsive aminopeptidase (IRAP) and modulates translocation of GLOT4 in the perinuclear region of adpocytes. It is an an effector in the insulin signalling pathway in eukaryotic cells. SPANK is useful for reducing body mass, reducing glucose intolerance or insulin resistance, for preventing
                                                                                                                                                                                                                                                                                                                                     SPANK; SAM; sterile alpha motif; PARP; insulin resistance; poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK; ankyrin repeat; cytosol, insulin-responsive aminopeptidase; IRAP; GLUT4; adipocyte; insulin signalling pathway; hyperlipidaemia; glucose intolerance; atheromatous disease; atherosclerosis; obesity; cardiac insulficiency; coronary insulficiency; stroke; high blood pressure; non-insulin dependent diabetes; hypertension; hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds.
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                                               3721 GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTG
                              GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTG
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/transl_except= (pos:1695. .1823,aa:482. .524)
/transl_except= (pos:2172. .2282,aa:641. .677)
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or treating obesity-related diseases or disorders, such as obesity, cardiac insufficiency, coronary insufficiency, stroke, hypertension, atheromatous disease, atherosclerosis, high blood pressure, non-insulin dependent diabetes, hyperlipidaemia, hyperuricemia and Syndrome X and is also useful for preventing or treating muscle-related diseases or disorders, such as muscular dystropphy, muscle atrophy and muscle fatigue. Antibodies immunospecific for SPANK are useful for detecting the presence of SPANK polypeptide in a biological sample
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Matches 3807; Conservative
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1328 AACGAATGCTATTTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGATG
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Best Local Similarity 99.8%; Pred. No. 0;
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                                                                                                              Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

99.4%; Score 3791.4; DB 5; Length 4406;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4406 BP; 1268 A; 910 C; 1054 G; 1174 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       New tankyrase2 polypeptides, useful for treating conditions poly(adenosine diphosphate-ribose) polymerase activity e.g. inflammatory and autoimmune disorders.
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                                                                                                                                                                                                                                                           Mcelligott
                                                                                            oligonucleotide SEQ
                                                                                                                                                                                                                                                          Goldman PS,
                                                                                                                                                                                                                                                                                                                                              Example 2; Page 168-173; 242pp; English
                                                                                            Human tankyrase2 clone consensus
                                    AAF63930 standard; DNA; 4406
                                                                                                                                                                                                                                                         Christenson E, Demaggio AJ,
                                                                                                                                                                                                  28-JUN-2000; 2000WO-US017827.
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                                                                        (first entry)
                                                                                                                       inflammatory disorder; ds
                                                                                                                                                                                                                                                                             WPI; 2001-102896/11.
                                                                                                                                                                                                                                                                                      P-PSDB; AAB66290.
                                                                                                                                                                                                                     29-JUN-1999;
                                                                                                                                           Homo sapiens
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                                                                                                                                                                                              GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAGCAGCAGTG 3845
                     CTGGTAGGCCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGAGAAC 3660
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inflammatory disorder; ds.
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ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory
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99.4%; Score 3791.4; DB 5; Length 5002;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                          Sequence 5002 BP; 1456 A; 1065 C; 1196 G; 1285 T; 0 U; 0 Other;
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New tankyrase2 polypeptides, useful for treating conditions mediated poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders.

The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-

5; Page 185-190; 242pp; English

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The specification describes a method for identifying a candidate adenomatous polyposis coli protein (APC) and axin pathways modulating agents. The method comprises providing an assay system comprising the assay system comprising the assay system with a test agent under conditions where, except for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system, where a difference between the test agent-biased activity and the reference activity identifies the test agent-biased activity and the reference activity identifies the test agent as a candidate APC and axin pathways modulating agent. The method is useful in identifying a candidate adenomatous polyposis coli protein (APC) and a pathways modulating agent, which are useful for preparing a composition for diagnosing or treating cancer. The present sequence encodes a human orthologue of a cancerbabditis elegans MAPCAX polypeptide. The sequence was identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a candidate adenomatous polyposis coli protein (APC) and axin pathways modulating agent for treating cancer by contacting an assay system comprising a modifier of APC and axin polypeptide or nucleic acid with a test agent.
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                                                                             29-JAN-2003; 2003US-0443484P.
11-FEB-2003; 2003US-0447358P.
10-APR-2003; 2003US-0461789P.
14-MAY-2003; 2003US-0470664P.
19-JUN-2003; 2003US-0479650P.
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                             28-JAN-2004; 2004WO-US002338
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Best Local Similarity 99.8
Matches 3806; Conservative
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P-PSDB; ADR14792.
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                                                           AGTCTGTGGAGGAAGAAGATACAGTTCGAGAGAGAGAGATGCAGAG
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                             <u>AGTCTGTGGAGGAAGAAGTGCAAAGTACAGTTCGAGAGCACACAGAGATGGAGGTCATGCAG</u>
                                                                                                                                         GTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTAT
                                                                                                                                                                          GTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTAT
                                                                                                                                                                                                                                                       GGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAAGAAAACCACAACCATGCCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of human MAPCAX orthologue #24.
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380. 3880
/*tag: a
/product= "MAPCAX orthologue"
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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosis is based on the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an optime polypeptide, preferably humanised or human; an anti-idiotype, non-human (moncolonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using NNA microstrays,
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3, Bruemmendorf T, Kinnemann H, Roepcke S;
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sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained atrongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR6554 represent the polymucleotide and polypeptide sequences used in the method of the
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches
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336 TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGCGGCGCGGATCATGTCGGGTCGCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Cor the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the colypeptide, preferably humanised or human; an anti-idotype, non-human or monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or canocin projectope. The polymulacidides are identified in human prostratic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concerpation of the antibody, atreptavidin-conjugated horseradish beroad antibody, streptavidin-conjugated horseradish concerpations and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue) and samples very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the confusional and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the horseral procession and cytoplasmic staining was very strong, and horseradical and polypeptid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
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Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
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Pred. No. 0;
0; Mismatches
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14-MAY-2003; 2003DE-01022134
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Best Local Similarity 99.8%;
Matches 3806; Conservative
        22-FEB-2004; 2004WO-DE000433
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                                                                                                                                     (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
                                                                                                                                                                   DAHL E.
ROSENTHAL A.
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                                                                                                                                                                                                                                                 (PILA/) PILARSKY C.
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                                                     Seguence 6189 BP; 1772 A; 1233 C; 1386 G; 1798 T; 0 U; 0 Other;
                                                                                                                            Query Match 99.4%; Score 3791.4; Best Local Similarity 99.8%; Pred. No. 0; Matches 3806; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A poly(ADP-ribosyl)ation polymerase (PARP) inhibitor of activity of an enzyme that mediates repair of a DNA strand break, useful in treating diseases with gene defects on homologous recombination.
                                                                                                                                      CTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCA
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This invention relates to novel tricyclic lactam indole and benzimidazole compounds that inhibit the activity of polyadenosine diphosphate (ADP)-
compounds that inhibit the activity of polyadenosine diphosphate (ADP)-
compounds that inhibit the activity of polyadenosine diphosphate (ADP)-
compound to a gene encoding a great a genetic defect
compound (HR), cancer i.e. a gene-linked hereditary cancer such as where the cancer cells are partially or totally deficient in BRCA1 and/or BRCA2 expression and to induce apoptosis in HR defective cells. The present invention describes this method as a stand alone therapy that conventional radiotherapy or chemcherapy treatments, avoiding the conventional radiotherapy or chemcherapy treatments, avoiding the effects. Furthermore, only low doses of these compounds need to be used hence reducing systemic build up and minimizing toxic effects. Accordingly, such compositions exhibit cytostatic activity and compositions as PARP inhibitors. This polynucleotide sequence is the DNA sequence of human tankyrase-2 mRNA, given in an exemplification of the invention.
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                             New tricyclic lactam indole and benzimidazole compounds are poly adenosine diphosphate-ribose polymerase inhibitors used for treating e.g.
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99.4%; Score 3791.4; DB 14; Length 6189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6189 BP; 1772 A; 1233 C; 1386 G; 1798 T; 0 U; 0 Other;
                                                                                          Disclosure; SEQ ID NO 5; 58pp; English.
WPI; 2005-162931/17.
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16-APR-2004; 2004GB-00008524
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Human, colon cancer-associated polypeptide, immune response; therapy; colon cancer; gene; ds.
                                      Human colon cancer-associated polypeptide gene, TNKL (BC-203)
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associated polypeptides as antigens that elicit immune response in colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for diagnosing colon cancer in a subject which comprises identifying colon cancer-associated polypeptides as antigens that elicit immune response in colon cancer. The method is useful for diagnosing, determining onset, progression, or regression of colon cancer in a subject, or for selecting a course of treatment of a subject having or suspected of having colon cancer. The colon cancer, and for following the course of treatment of cancer, and for following the course of treatment of colon cancer, and for following the course of treatment of colon cancer is human colon cancer-associated polypeptide gene
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TAGCAGCTCTACTAATAAAGTATAATGCATGCTCAATGCCACGGACGAATGGGCTTTCA CACCTTTGCACGAAGCAGCCAAAAGGCCACGGACGAATGGGCTTTCA CACCTTTGCACGAAGCACAAGGCACGACGATGCTTTGTGCTTTGTTGCTTTCACCC CACCTTTGCACGAAGCCCAAAAGGACGAACAACACTTTGTTGCTTGC	2764 GTTTTCAGAACTGTCTTCAGTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTTTGG 2823 [2884 TTGAGCACCTAATGGATATTTGACAGAACAGATCACTTTGGATGTATTAGTTGGA 2943	3004 TTAAAGGAGTCGAGAACTTATCTCCGGACAACAAGGTCTTAACCCATATTTAACTTTGA 3063	Qy 3124 CTGTGGAGGAAGAATGCAAAGTACAGTTCGAGAGCACAGAGATGATGGAGGTCATGCAGGTG 3183 Db 3120 CTGTGGAGGAAGAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGGTG 3179 Qy 3184 GAATCTTCAACAGATACTCTCAAGATTCAGAAGGTTTGTAACAAGAACTATGGG 3243 Db 3180 GAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAACTATGGG 3239	AAAGATACACTCACGGGGAAAAGAAGTTTCTGAAGAAAACCACAACCACAACCAAC	OY 3364 GGCATGCGTACATAGGTGATTTTGGAGCTGGCATTTATTT	Oy 3424 AAAGCAATCAATATGTATATGGAGGAGGGGTACTGGGTGTCCAGAAGACA 3483 Db 1400 AAAGCAATCAATATGTATATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAAGACA 3479 Oy 3484 GATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTCTT 3543 Oy 1000 AAAACTTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGTCTT 3543

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Unknown.
Unclassified.
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Luo,Y., Chan,E., Xu,X., Huang,B. and Ossovskaya,V.
Tankyrase H, compositions involved in the cell cycle and methods of
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Rigel Pharmaceuticals, Inc.; South San Francisco,
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AFTPLHEAASKNRVEVLLLSYGADPTLLNCHKSAIDLAPPPQLKERLAYEFKGHS
LLQAAREADVTRI KKHLSLEWNNFKHPQTHETALHCAASPYPRKKQI CELLLAKKGAN
INEXTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCR
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KLCTVQSYNKRDI BGRQSTPLHFARGYNN VSVPTLLQHGADVHAKNGGGLVPLHNA
CSYGHYEVAELLVRGGAVNVNADJNKFTPLHBAAKGKEI CKLLLQHGADPTKORD
GNTPLDLVRGGDTDI QDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTP
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TDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAM
PPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVS
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1. (bases I to 6028)

Chi, N.-W. and Lodish, H.F.

A novel homolog of Tankyrase

Onbubblished
                                     3661 AGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTGGTG
                                                                                                         GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCGTCATGAGCAGCGGGG
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                                                                                     GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTG
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Chi.N.-W. and Lodish,H.F.
Chi.N.-W. and Lodish,H.F.
Submission
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Research, 9 Cambridge Center, Cambridge, MA 02142, USA
Location/Qualifiers
1. 6028
/organism="Homo sapiens"
/mol.type="mRNA"
/db_ref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                             6028 bp mRNA linear P.
Homo sapiens tankyrase-2 (TNKS-2) mRNA, complete cds.
AF309033
                                                                                                                                                        GCCTCTACGTTTTACTCCTTTGCTGAAAAAAAAA 3816
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/note="STS WI-16054"
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/gene="TNKS-2"
252. 3752
/gene="TNKS-2"
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                                                                            TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGCGGCCAGGATCATGTCGGGGTCGCCGCT
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                                    Length 6028;
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                                   Query Match 99.4%; Score 3793; D
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3807; Conservative 0; Mismatches
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/gene="TNKS-2"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                        GGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAAGAAAACCACAACCATGCCAATG
                                                                                       GGGAAAGATACACTCACCGGAGAAAGAAGTTTCTGAAGAAAACCACACCATGCCAATG
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A novel insulin signaling molecule
Patent: WO 0077225-A 2 21-DEC-2000;
WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; THE (HOSPITAL CORPORATION (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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            3268 GGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAAGAAAACCACAATGCCAATG
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Second mammalian tankyrase

JAL Parent: US 659728-A 5 29-JUL-2003;

Geron Corporation; Menlo Park, CA

Location/Qualifiers

source //organism="unknown"
//mol_type="genomic DNA"
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            ATGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTT
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TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGGATGTTACTC TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC GAATCAAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACATGAAA GAATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACATGAAA CAGCATTGCATT	1440 TGCTAAGAAAAGAACAACAATCAATGAAAAGACTAAAGAATTCTTGACTCCTGCAGCG 1499 1441 TGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGGTGAAACATGAAGCAAAGG 1500 1500 TGCATCTGAGAAAGCTCATAATGATGTTGTTGATGTGGTGAAACATGAAGCAAAGG 1559 1501 TTAATGCTCTGGATAATCTTGGTCAACTTCTCTAACACAGAGCTGCATATTGTGGTAACATGAAGTAATGATGATGATGATAATGATGATGATAATGATG	1561 TACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG 1620	1681 CATTAGGTAATTCAGAGCAGACAGACAGAGAGCTGGAAAGCTGGAAAGGTTGC 1740	1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGC 1860	1921 CATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA	41 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTACCAAAAAAAA	2101 ATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTTGGAGGAGG 210, 2160 ATACTCCTTTGGATCTTGTTAAAGATGGAGATACTGATTTCAAGATCTGCTTAGGGGAG 221, 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAAGAAGTGAAGAAGTTGTTT 222, 21220 ATGCAGCTTTGCTAGATGCTGCCAAGAAGGGTTGTTTAGCCAAGAAGAAGAAGTTGTCTT 222,	2221 CTCCTGATAATGTAAATTGCCGGATACCCAAGGCAGACATTCAACACCTTTACATTTAG 228
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MVNFKHPQTHETAHACAAASPKPRKQI CELLLKKGANI NRKTKEFLTPLHVASEKAH
NDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNI I SLQGFTAL
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                         CCAAAAGCAATCAATATGTATATGGAATTGGAGGTACTGGGTGTCCAGTTCACAAG
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GATADALSSESSELSSELASSELDLESSVSSSGFTEGASSERKEVPEVDF
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OFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGWVDG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Patent: WO 100849-A 134 04-JAN-2001;
ICOS CORPORATION (US)
Location/Qualifiers
3126 IGAACACCTCTGGTAGTGGAACAATTCTTATAGATCTGTCTCCTGATGATAAAAGAGTTTC
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                               661 AIGGAGCIGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATC
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
Tankyrase2 materials and methods
Parent: WO 0100849-A 132 04-JAN-2001,
ICOS CORPORATION (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="unnamed protein product"
      DNA
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Pred. No. 0;
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Sequence 132 from Patent WO0100849. AX062273 AX062273.1 GI:12540174
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Matches 3806; Conservative
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
CTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAAC
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Use of RNAi inhibiting parp activity for medicament for the treatment of cancer parent: WO 2005012524-A 8 10-FEB-2005; The University of Sheffield (GB)
                                                                                                                     CS019687 6189 bp DNA
Sequence 8 from Patent WO2005012524.
CS019687.1 GI:60220692
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    /db_xref="taxon:9606"

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Db 3816 AGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATG 3875 Qy 3721 GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTG 3780	REPERINTION SEQUENCE STOOM PARENT WOODSOIDSON. COCCURSON COCCURS

GCTTTACTGCTTTACAGATGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCT 1680 	<i>ે</i> જે જે જે	CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGCAGCCAGC
CATTAGGTAATTCAGAGGGGGGCAGACAATTGCTGGAAGCTGGCAAAGGCTGGAGATGTCG 1740 	& 8 —	2761 GGAGTITITCAGAACIGICTICAGTAGTICAAGTGGAACAGAGGGTGCTICCAGIT 2820
GCGTC 180	& g	2821 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG 2880
TCTGC 1860	& g	2881 GACTTGAGCACCTAATGGATATTTGAGAGAGACACATCACTTTGGATGTATTAGTTG 2940
192	& 4g	2941 AGATGGGGCACAAGGAGCTGAAGGAGATTGGAATGAATGCTTATGGACATAGGCACAAAC 3000
AGTTA 198	중 음	3001 TAATTAAAGGAGTCGAGACTTATCTCCGGACAAGAGTCTTAACCCATATTAACTT 3060
ATATG 204	상 염	3061 TGAACACCTCTGGTAGTAGAACAATTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTC 3120
TGGAA 210	& g	3121 AGTCTGGAGGAAGAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAG 3180
GGGAG 216	& a	3181 GTGGAATCTTCAACAGATACAATATTCTCAAGATTCACAAGGTTTGTAACAAGAACTAT 3240
ATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTTAGGGGAGGTTGTTTAGCCAGAGTGGAGAAGATTGTCTT 2220	oy Oy	3241 GGGAAAGATACACTCACCGGAGAAAGAAGTTTCTGAAGAAACCACAACCATGCCAATG 3300
TTTAG 2280	& g	3301 AACGAATGCTATTTCATGGGTCTCCTTTTGTCAATGCAATTATCCACAAAGGCTTTGATG 3360
TGTGA 234	& 8	3361 AAAGGCAIGCGIACAIAGGIGGIAIGIIIGGAGCIGGCAITIAITITIGCIGAAAACICIT 3420
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3GGCTT 2460	& g	3481 ACAGATCTTGTTACATTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAGT 3540
GCTAG 252	λ ₀ α ₀	3541 CITICCIGCAGITCAGIGCAAIGAAAAIGGCACAITCICCICCAGGICAICACTCAGICA 3600
GCTAG 267	çy Op	3601 CTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAAC 3660
CTCTT 264	\$ a	3661 AGGCTTATCCTGAGTATTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATG 3720
CTCTCT 279	<i>ኤ</i> 8	3721 GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGGGGGGGG
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TEEKVNSRDTAGRKSTPLHFAAGFGRKDVUSYLLQNGANVQARDDGGLI PLHHACSFG
HAEVVNLLIARRGABDNARDNWYYTPLHEAAT KGKIDVCI VLLQHGAEPTIRNTDGRTA
LDLADPSAKAVTGEYKGDELLESARSGNERGOMALLTPLANNCHASDGRKSTPLHLA
AGYNRVKI VQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLW
QFTPLHEAASKNWYSVCSLLLSYGADPTLLNCHNKSAI DLAPTPGLKRRLAYERKGHS
LLQAAREADVTRIKKHLSLEWWYNKHPQTHTALHCAAAS TDRAPTPGLKRLAYERKGHS
ILLBYGCDPNI ISLQGFTALQMGNBNVQQLLQEGI SGLGNSEARRAYCGHLQTCR
ILLSYGCDPNI ISLQGFTALQMGNBNVQQLLQEGI SGLGNSEARRACGDVETV
KKLCTVQVNVCRI BERQGSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNA
CSYGHYEVALLVKHGANVNVADLAKETPLHEAAAKKKYEICKLLGHGADPYRKNRD
GYTPLDLVKDGDTDI QDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRISTP
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QSPYREHRDGGHAGGIFNRYNILKIQKVCNKKLWBRYTHRRKEVSEENHNHANERMLF
HGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKDRS
CYICHRQLLFCRYTLGKSFLQFSAMKWAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ
AYPEYLITYQIMRPEGMVDG"
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PDKWAFTPIEDLAVADDVSALLITAAM
PDRAALPESAQKGRYDCALLLAHGADPTLAKOGGOGTDLDVSADDVSALLITAAM
PDRAALPSCYKRQVIGVORSPGATADALSSGPSSSSSLSAASSLDNLSGSFSELSSVVS
SSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Location/Qualifiers

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/note="telomerase binding pr
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Db 2496 ATGCCCAAGAGAGGACTTATTCCTTTACATAATGCAGCATCTTAGGGGCATGTAG Qy 2401 ATGTAGCAGCTCTACTAATAATGCATGTGTCAATGCCACGGACAAATGGGGTT	Db 2616 TCACACCTTTGCACGAAGCAGCCCAAAAGGGACGAACACACAC	2581	2641	2701	2761	2821	Cy 2881 GACTTGAGCACCTAATGGATATTTGAGAGAGACGATCACTTTGAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	Oy 2941 AGATGGGGCACAAGGGCTGAAGGAGATTGGATTCATGTTATGGACATAGCCACAAAC	Qy 3001 TAATTAAAGGAGTCGAAGACTTATCTCCGGACAACAAGGTCTTAACCTTTAACTT		Qy 3121 AGTCTGTGGAGGAGAGAGAGTACAGTTCCAGAGGACAGAGATGGAGGTCATGCGG 	Qy 3181 GTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTAT	Oy 3241 GGGAAAGATACACTCACCGGAAAAAGAAGTTTCTGAAGAAACCACACCATGCCAATG	Qy 3301 AACGAATGCTATTCATGGGTCTCCTTTTGTGAATGCAATTATCCACAAAGGCTTTGTG 	Qy 3361 AAAGGCATGCGTACATAGGTGTATGTTTGGAGCTGGCATTTATTT	Qy 3421 CCAAAAGCAATCAATATGTATATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAAG
		TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATC 156	1561 TACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCTTCAGG 1620 	1621 GCTTTACTGCTTTACAGATAGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCT 1680 	1681 CATTAGGTAATTCAGAGGCAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCG 1740 	1741 AAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGCGTC 1800 	1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGAATATCTGC 1860 	AATG 192	CATGITCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA	TATG 204 TATG 219	2041 ADAITTGCAAACTTCTGCTCCAGCATGCAGACCCTACCAAAAAAAA	2101 ATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGGG 2160 	T	2221 CTCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGACATTCAACACCTTTACATTTAG 2280 	234	GTAG 240

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                                                    540 TCAATCTCCTTTTGCGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATACTC
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                                       364 AGAAGGTGAACAGCCGCGCACACGGCGGGCAGGAAATCCACCCCGCTGCACTTCGCCGCAG
                                                                                        GITITGGGCGGAAAGACGTAGITGAATATTTGCTTCAGAATGGTGCAAATGTCCAAGCAC
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Chen Y.-T., Old'L.J., Scanlan,M.J. and Stockert,E.
Colon cancer antigen panel
Patent: US 6794501-A 11 21-SEP-2004;
Ludwig Institute for Cancer Research and Cornell F
Foundation, Inc.; New York, NY
Location, Location/Qualifiers
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l & A	TTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCCTCCAAGAGGGTATCTCAT 168 TTACTGCTTTACAGATGGGAAATGAAATGAAATGAACAGAACTCCTCCAAGAGGGGTATCTCAT 167 TTACTGCTTTACAGATGGAAATGAAATGAAATGAACAGCAACTCCTCCAAGAGGGGTATCTCAT 167	& a	2704 CAGGTCCATCTAGCCCATCAAGCCTTTCTG(
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è 4	CTGATAATGTAAATTGC 	& A	3304 GAATGCTATTTCATGGGTCTCCTTTTGTGAA
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& q	2344 CCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAGATG 2403 	රු දු	3424 AAACCAATCAATATCTATATTGAATTGGAG
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2639 2703 2699 TCAAGTGGAACAGAGGTGCTTCCAGTTTGG 2823 AGCATAACTCAATTCGTAAGGAATCTTGGAC 2883 ATCAATGCTTATGGACATAGGCACAAACTAA 3003 CGAGAGCACAGAGATGGAGGTCATGCAGGTG 3183 ATTCAGAAGGTTTGTAACAAGAAACTATGGG 3243 2643 2763 2759 GATCTGTCTCGTGATGATAAAGGTTTCAGT 3123 CTCTTTTGCCGGGTAQCCTTCGGAAAGTCTT 3543 CATTCTCCTCCAGGTCATCACTCAGTCACTG 3603 AGCCCAGGAGCCACTGCAGATGCTCTCTT

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TGGGCGCGCCCATGGGACTGCGCCCGGATCCGGTGACAGCAGGGAGCCAAGCGGCCCCGGG
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ARDNWAYPTPHEAAI KKKI DVCIVLLQHGAEPTRINTDCRTADLADBSARAVITGEY
KKDELLESARSGNEEREKWALLIPLNNYCHASDGRKSTPLHLAAGYNRVKI VQLLLQHG
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VNVVADLMKFTPLHEAAAKGKYEICKLLLQHGADPJRKNRDGHTPLDLVKDGDTDIQD
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protein mRNA, partial cds.
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arvgghgtapdpvtagsqaaralsasspgglalllagpclllrllalalaarims
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 3748 GGATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGT 3807
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 4295)

Monz, D., Munnia,A., Comtesse,N., Fischer,U., Steudel,W.I.,
Felden,W., Glass,B. and Meese,E.U.
Novel tankyrase-related gene detected with meningioma-specific of the concer Res. 7 (1), 113-119 (2001)
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Submitted (12-SBE-2000) Human Genetics, Universitaet
Saarlandes, Geb. 60, Homburg 66421, Germany
Location/Qualifiers
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                                                                   3808 GGCCTCTACGTTTTACTCCTTTTGCTGAAAAAAA 3841
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens tankyrase-related <sub>I</sub>
AF305081
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Monz, D.W. and Meese, E.
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Best Local Similarity 99.6%;
Matches 3798; Conservative
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<u>9</u> g	3435	GAAAGGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTT
ٷ	3420	TCCAAAAGCAATCAATATGTATATGGAAGTACTGGGTGTCCAGAA 3479
qq	3495	
ò	3480	GACAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGGTAACCTTGGGAAAG 3539
qq	3555	GACAGATCTTGTTACATTTGCCACAGGCAGCTGCTCTTTTGCCGGGTAACCTTGGGAAAG 3614
ò	3540	TCTTTCCTGCAGTTCAGTGCAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTC 3599
QQ	3615	TCTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTC 3674
ò	3600	ACTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGCTGAATATGTTATACAGAGAGAA 3659
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qq	3735	CAGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGAT 3794
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qq	3795	GGATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCCATCAAAGCAGCAGT 3854
ò	3780	GGCCTCTACGCTTTTACTCCTTTGCTGAAAAAAA 3813
Ωp	3855	

Search completed: December 19, 2006, 00:40:58 Job time : 20642.4 secs

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	0 2 2 2 5 2 4 4 2 6 6						RESULT 1 AK047094 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL PURMED	REFERENCE AUTHORS	JOURNAL	REFERENCE AUTHORS		TITLE JOURNAL PUBMED	REFERENCE AUTHORS TITLE
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GenCore version 5.1 Copyright (c) 1993 - 2006 Bic	 nucleic search, using sw model December 18, 2006, 13:00:27; sc (with 	US-10-616-101-2 =: 3816 1 cgcgctcgccgccgc	le: IDENTITY_NUC Gapop 10-0 , Gapext 1.0 48236798 segs. 27959665780 residues	ts satisfying chosen para	seq length: 0 seq length: 2000000000	sing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	EST:* 1: gb_est1:* 2: gb_est3:* , 3: gb_est4:* 4: gb_est5:* 5: gb_est6:* 7: db_est6:*	95 68 E E E E E E E E E E E E E E E E E E	No. is the number of greater than or equa; derived by analysis	* Query re Match Length DB ID	.4 43.6 .8 42.2 .8 38.8	.2 37.6 3194 6 .6 33.3 3612 14 .2 23.4 3107 14	.4 23.2 888 8 .6 22.5 926 8 .2 20.6 838 1 .2 20.4 1078 6	.6 20.2 898 .8 20.1 834 .9 18.6 848 .8 18.2 819 .8 18.0 955	.4 17.6 675 4 .2 17.6 1128 2 .2 17.4 754 4 .4 17.3 663 9
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ALIGNMENTS

AK047094

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AK047094

Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930018021 product.TANKYRASE-RELATED PROTEIN (FRAGMENT) homolog (Homo sapiens), full insert sequence. AK047094.1 GT:26338577

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house)

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AUTHORS JOURNAL REFERENCE

TITLE

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LLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGASLGHSEADRQLLEAAKAGDVFTV
KKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNA
CSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAA"
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                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)
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                                                                  The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
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/ hote="unnamed protein product; TANKYRASE-RELATED PROTEIN
(FRAGMENU) homolog [Homo sapiens] (SPTR|Q9HAS4, evidence:
FASTY, 94.6*ID, 51.4*length, match=1959)
                                                                                                                      Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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AK048860 3417 bp mRNA linear HTC 02-SEP-2005 Mus musculus O day neonate cerebellum cDNA, RIKEN full-length

RESULT 2
AK048860
LOCUS
DEFINITION

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The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

Genome Science Group (Genome Network Project Core Group).

The Transcriptional Landscape of the Mammalian Genome.

Science 309, 1559-1563 (2005)

B (bases 1 to 3417)

B (bases 1 to 3417)

S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haranco, K., Hiramco, M., Hiramco, M., Hiramco, M., Hiramco, M., Hiramco, T., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Sasito, R., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Šasaki, D., Shibata, K., Tanaka, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Taya, T., Yasunishi, A., Takada, Y., Tanaka, T., Taya, T., Yasunishi, A., Tayawa, A., Takahashi, R., Takada, Y., Tanaka, T., Taya, T., Yasunishi, A., Tayawa, A., Tayawa, A., Takahashi, A., Takahisa, S., Tanaka, T., Tayawa, A., Tayawa, A., Tayawa, A., Yasunishi, A., Tayawa, A., Tayawa, A., Yasunishi, A., Tayawa, A., Tayawa, A., Yasunishi, A., Tayawa, A., Yasunishi, A., Tayawa, A., Yasunishi, A., Tayawa, A., Tayawa, A., Yasunishi, A., Tayawa, A., Tayawa, A., Yasunishi, A., Tayawa, A., Yasunishi, A., Tayawa, A., Tayawa, A., Yasunishi, A
enriched library, clone:C230076L23 product:tankyrase,
TRF1-interacting ankyrin-related ADP-ribose polymerase, full insert
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Direct Submission
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HTC; CAP trapper.
Mus musculus (house mouse)
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
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Hardnggripplhaacsyghtstrikenacunadumopfplheraaskrriveucsi
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tankyrase, TRF1-interacting ankyrin-related ADP-ribose
polymerase (MGD|MG1:1341087 GB|AA415426, evidence: BLASTN,
99%, match-439)
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mol_type="mnNA"
strain="CS7BL/65"
/db_xxef="taxon:10090"
/clone="C230076L23"
/tissue type="cerebellum"
/clone_Tib="RIKEN full-length end
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/db_xref="G1:26339608"
                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
AAACTATGGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAAGAAAACCACAAACAT 3293
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
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Mus musculus (house mouse)
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Nature 420 (6915), 563-573 (2002)
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38.8%; Score 1481.8;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 1591; Conservative 0; Mismatches
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://fantom.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Pax:81-45-503-9216)
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POLYMERASE homolog [Homo sapiens] (SPTR|095271, evidence:
FASTY, 95.9%ID, 80%length, match=3167)
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The Transcriptional LandScape of the Mammalian Genome Science 309, 1559-1563 (2065)

B (bases 1 to 3194)

Radachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Rukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiramco, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Salto, R., Sakai, K., Sakai, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Murametsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                        enriched library, clone:B430206N15 product:TRF1-INTERACTING
ANKYRIN-RELATED ADP-RIBOSE POLYMERASE homolog [Homo sapiens], full
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea; Muridae, Murinae, Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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                                                                                                                                                                                                                                                                          852 AGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTG
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                                                                                                          GAAGAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGCAAGTGATGGC
                                                                                                                                                                                                                                                                                                                                                                                       912 TTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGGTACCATTACAC
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                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheleen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                           Hominidae, Homo.

1 (bases 1 to 3612)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.,Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans a
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sapiens TNKS gene, VIRTUAL TRANSCRIPT, partial
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/organisma"Homo sapiens"
/mol_typea"genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
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1 (bases 1 to 3107)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B. Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                            GGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGAGAGACTTATCTCC
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                                                                                                                                                                                                                                                  White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and orderin them based on alignment. Translation starts at the beginning alignment.
                                                                                                                                                                            63;
                                                                                                                                                          Length 3107;
                                                                                                                                                                           0; Mismatches 1255; Indels
                                                                                                                                                         DB 14;
                                                                                                                                                        Score 892.2; DB 14
Pred. No. 1.5e-223
                                                              Location/Qualifiers
1. 3107
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                            <1. ... > 3107
/gene="TNKS"
/locus_tag="HC3703"
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Best Local Similarity 49.2%;
Matches 1275; Conservative
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RZPDD; RZPDD1816; (Human T-Lymphocytes) RZPD LIB No.9017
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:
Inge Arlart
RZPD Deutsches Reseourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD99017K2313
contact RZPD (product support@rzpd.de) for further information.
Primer name: qe3 4, Primer sequence: CGGATAACAATTCACACAG.
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                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                CTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGAG 3017
                                                                                                                                                                                                                                                                          AGACTTATCTCCGGACAACAAGGTCTTAACCCATATTAACTTTGAACACCCTCTGGTAGT 3077
                                                                                                                                                                                                                                                                                                                                                                                                                                3138 ATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGGTGGAATCTTCAACAGA 3197
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1 (bases 1 to 888)
Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D. and Korn,B.
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                                          2838 CCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATG
                                                                                3198 TACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTATGGGAAAGATACACTCAC
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Unpublished (2005)
Contact: Inge Arlar
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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720 CCTTTACATAATGCAGCATCTTACGGGCATGTAGATGTANCAGCTCTACTAATAAAGTAT
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RZPD Deutsches Reseourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 110
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016I1435
contact RZPD (product support@rzpd.de) for further information.
Primer name: q63 4, primer sequence: CGGATAACAATTCACACAG.
Location/Qualifiers
                                                                                                  GCAGGTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAA 3236
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1 (bases 1 to 926)

Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPDP, STROPPOSIGI1435.
RZPDP, RZPDP, STROPPOSIGI1435.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
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                                 TITCAGTCTGTGGAGGAGAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCAT
                                                             TTTCAGTCTGTGGAGGAAGAGTGCAAGTACAGTTCGAGAGACACAGAGATGGAGGTCAT
                                                                                                                                GCAGGTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAA
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/note="Vector: pQE80LSN_cloned; Site_1: Sal1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                       3417 TCTTCCAAAAGCAATCAATATGTATATGGAATTGGAGGTACTGGG 3464
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/db_xref="taxon.9606"
/clone="R2PDp901611435"
/tissue_type="T-Lymphocytes"
/dev stage="adult"
/lab_host="DH108"
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Mus musculus 2 cells egg cDNA, RIKEN full-length enriched library, clone:B020015H19 product:Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase 1) (TANK2) (TANK2) (TRIKY-3) (TANK2) (TRIKY-3) (T
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                   241 TCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGAGAGACTTATCTCCGGAC
                                                                                                                                                                      301 AACAAGGTCTTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAG
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2974 TCAATGCTTATGGACATAGGCACAACTAATTAAAGGAGTCGAGAGACTTATCTCCGGAC
                                                                                                                                      3034 AACAAGGTCTTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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I (bases I to 838)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
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                                                                                                                                                                                                                                                                     AU140145 AUG-2002 838 bp mRNA linear . EST 05-AUG-2002 AU140145 PLACE2 Homo sapiens cDNA clone PLACE2000021 5', mRNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: flj-cdnamifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-396
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Pred. No. 3.4e-195;
0; Mismatches 13;
                               2547 AATCAGGAAGGACAAACACCTTTAGATTTA 2576
                                                                      896 AATCAGGAAGACAACNCCCTTTAAATTTA 925
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/db_xref="taxon:9606"
/clone="PLACE2000021"
/tissue_type="placenta"
/clone lib="PLACE2"
/note="Vector: pME18SFL3"
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Genome Res. 16 (1), 55-65 (2006)
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Best Local Similarity 98.0%;
Matches 823; Conservative (
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                          Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Arawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bano,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gasterland,T., Glssi,C., King,B., Kochiwa,H.,
Kuchi,P., Lewis,S., Matsuo,Y., Nikaldo,I., Pesole,G.,
Ruehi,P., Lewis,S., Matsuo,Y., Nikaldo,I., Pesole,G.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bolinga,N.,
Fletcher,C., Fulita,M., Gariboldi,M., Gustincio,R., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Narchionni,L., Mashima,J., Mazzarelli,J., Mombaerte,P.,
Sato,K., Schonbach,C., Seya,T., Shibatta,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L.,
Marchia, V., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Kiyosawa,H., Yagai,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarali,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schrimi,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Belsel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Gaasterland,T.,
Gariboldi,M., Gisel,C., Godzik,A., Gaosterland,T.,
Gariboldi,M., Gisel,C., Godzik,A., Gough,J., Grimmond,S.,
Gariboldi,M., Gisel,C., Godzik,A., Gough,J., Grimmond,S.,
Kawaji,H., Kawasawa,Y., Kedzlerski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Ring,B.Z., Kingwald,M.,
Sandelin,A., Schneider,C., Setou,M., Shimada,K.,
Vang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Wells,C., Wilming,L.G., Wanghese,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wanghaw-Boris,A., Carninci,P.,
Rawawa,T., Fukuda,S., Hara,M., Kawan,J., Alzawa,K.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Sokhino,M., Waterston,R., Lander,B.S.,
Rogers,J., Birney,E., and Hayashizaki,Y.
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Nature 420 (6915), 563-573 (2002)
                          Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Sumi, N., Ishil, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Hayashizaki,Y.
RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Bannal, W., Baxter, L., Neden, K., Bersan, C., Souch, C., Chair, C., Conce, M. L., Dillas, D., Dellas, D., Dellas,
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990 900

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DT808067 898 bp mRNA linear EST 12-OCT-2005 LB0173.CR_I04 GC_BGC-17 Bos taurus cDNA clone IMAGE:8121774 5', mRNA sequence.
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/dev_stage="6 months old fetus"
/dev_stage="6.coli DH10B T1 Phage Resistant"
/clone_lib="GC_BGC-17"
/note="Organ: Ascending colon; Vector: pExpress 1; Site_1:
Blunt (5' end of cDNA); Site_2: NotI (3' end of cDNA)"
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1 (baee 1 to 898)

Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaiff, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J. Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A. Bovine Genome Sequencing Program: Full-length cDNA Sequencing Unpublished (2005)
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                     ATTIGGCAGCAGGATATAACAGAGTAAAGATIGTACAGCTGTTACTGCAACATGGAGCTG
                                                                                                    931 ATGTCCATGCTAAAGATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTC
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Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
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20.2%; Score 770.6; DB 10; Length 898;
Best Local Similarity 92.1%; Pred. No. 1.4e-191;
Matches 824; Conservative 0; Mismatches 69; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
                                                                                                                                                                               ATTATGAAGTAACTGAACTTTTGGTCAAGCA 1021
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/organism="Bos taurus"
/mol_type="mRNA"
/strain="L1 Hereford"
/db xref="taxon:9913"
/clone="IMAGE:8121774"
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Fax: 1-604-876-3561
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                                                                                            /cione="B020015H19"
/tissue_type="egg"
/cione_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="2 cells"
1. .1078
                                                                                                                                                                                                                        (TNKS-2) (TRF1- interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like protein) (Tankyrase-related protein) homolog [Homo sapiens] (UniProt |Q9H2K2, evidence: PASTY, 94.7%ID, 22.7%length, match=794)
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/db_xref="taxon:10090"
organism="Mus musculus"
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Best Local Similarity 91.1
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Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Caniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

[ Dases I to 814)
Smith, T. P. L., Grosse, W. M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M. P., Laegreid, W. W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertes, G., Holt, I., Karamycheva, S., Liang, F.,
Guackenbush, J. and Keele, J. W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
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   GICTTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAGATCTGT
                  GTCTTAACCCATACTTAACTCTGAACACCTCTGGAAGTGGAACAATTCTCATTGATCTGT
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Exa: 402 762 4366
Email: smith@email.marc.usda.gov
Emails smith@email.marc.usda.gov
single page sequencing: Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 98 row: I column: 7
Seq primer: GTAATACGACTATAGGG.
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//db_xref="taxon: pg13"
//db_xref="taxon: pg13"
//tissue_type="pooled"
//lab_host="DH10B"
//clone_lib="MARC 4BOV"
//clone_lib="MARC 4BOV"
//lab_host="yector: pCMV SPORT6; Site_1: NotI; Site_2: Sa_Library made_from pooled_tissue_from day_20 and_day_embryos."
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libraries and construction of a gene index for Genome Res. 11 (4), 626-630 (2001) 11282978
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                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
                                                            Contact: Smith TPL
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DA733094 NT2RP2 Homo sapiens cDNA clone NT2RP2002155 5', mRNA
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1 (bases 1 to 819)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Yoneyama, T., Satio, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Satio, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative
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Genome Res. 16 (1), 55-65 (2006)
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Helix Research Institute
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1 (Dases 1 to 848)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.99329.
Blate: RLK8064 row. G column: 17
Seq primer: GTAATACGACTATAGGG.
                                        1907 ACCTTTGCACAATGCATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACA 1966
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234 GGTGGAATATCTGCTGCAACACGGGGCTGACGTGCATGCGAAAGACAAAGGGCCTTGT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1967 TGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTTACATGAAGCAGCAGC
                                                                                                                                                              /note="Vector: pcDNA3.1; Site 1: EcoR1; Site 2: Not1; Library made with RNA pooled from multiple.tIssues including ovary, hindbrain, uterus, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1608 ATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTC
                                                                                      174 ACCTTTGCACAATGCATGTTCTTATGGACATTATGAAGTTGCAGAGCTTCTTGTTAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                            2027 AAAAGGAAAATATGAAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTAC 2080
                                                                                                                                                                                                                                                      54 CAAAGGAAAATATGAAATTTGCAAACTTCTGCTTCAGCATGGTGCAGACCCCAC 1
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1372517 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
DN536421 GI:60988240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.6%; Score 709; DB 9; L
Best Local Similarity 91.5%; Pred. No. 2.6e-175;
Matches 762; Conservative 0; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
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DN536421
LOCUS
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ORIGIN

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/clone lib="NHH MGC 164"
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/note="Vector: pCMV-SPORT6.1; Site l: NotI;
/notice="Vector: pCMV-SPORT6.1; Site l: NotI;
/notIt line line line line l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The musculus musculus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Rodentia; Sciurognathi; Murchafae; Murinae; Mus.

25 1 (bases 1 to 955)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Nupublished (1999)

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-rômail.nih.gov

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-rômail.nih.gov

Tissue procurement: Dr. David Rowe and Dr. Mina

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM0316 row: o column: 01

High quality sequence stop: 779.
                                                                                                                                                                                                                                                                                                CB183123 955 bp mRNA linear EST 31-JAN-2003 AGENCOURT 11385409 NIH MGC_164 Mus musculus cDNA clone IMAGE:30244272 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCTGAAGGAGATTGGAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTC 3014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2835 GTTCCAGGAGTAGATTTTAGCATAACTCCAATTCGTAAGGAATCTTGGACTTGAGCACTA
                                        720 TICCACACCTITACATTITAANCANCIGGITATAATAATTITAAAAATTGCAAAATATTITGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTCAGGAATCGATTTTAGTATAACTCAGTTCATAAGGAACCTTGGACTTGAGCACTTG
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2261 TTCAACACCTTTACATTT-AGCAGCTGGTTATAATAATTTAGAAGTTGCAGAGTATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 955;
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                                                                                                          2320 TACAACACGGAGCTGATGTGAATGCCCAAGACAAAGGAGG
                                                                                                                                                                 780 TACACCCNGAACTAATTTTAATGCCCCANAACAAAGGAAG
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88.5%; Pred. No. 1.1e-169;
ive 0; Mismatches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                      CB183123.1 GI:28181571 EST.
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Matches 768, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2201 CAGAGTGAAGAAGTTGTCTTCTCCTGATAATGTAAATTGCCGCGATACCCAAGGCAGACA 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGC 2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGGTGGAATATCTGCTACAGCATGGANCTGATGTGCATGCTAAAGGTAAAGGAGGCCT 360
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                               Tel: 81-438-52-3975
Sex: 81-438-52-3986
Email: flj-cdnagnifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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/db_xrefe="taxon:960"
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/coll_line="NT2"
/coll_line="YP2RP2"
/none="Vector: pME18SFL3; mRNA from NT2 neuronal pcells after 2-weeks retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
     2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 692.8; DB 9;
Pred. No. 4.8e-171;
0; Mismatches 52;
                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 93.0%;
Matches 763; Conservative (
                                                                                                                                                                                                                                                          .819
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	AGTGGAACAATT	GAGATGCAAAGT	GAGATGCAGAGT	AGATACAATATT	AGATACAACATT	CACCGGAGAAAA	CACCGGAGAAAA	CATGGGTCTCCT	CATGGGTCTCCT	ATAGGTGGTATG	ATAGGTGGCATG	TATGTATAT-GG	TATGTGTATNGG	CATTTGCCACAG	CATTTGTCACAG	CAGTGCAATGAA	CAGCGCAATGAA	TGTAAATGGCCT	TGTAAAT-GCCT	GTATTTAATTAC		
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Search completed: December 19, 2006, 01:59:26 Job time : 16891.5 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

; Search time 3873.64 Seconds (without alignments) 12104.784 Million cell updates/sec December 18, 2006, 17:00:29 Run on:

US-10-616-101-2 3816 Title: Perfect score:

Seguence:

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

Searched:

37784340 Total number of hits satisfying chosen parameters:

18892170 segs, 6143817638 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 5, Appli	Sequence 106, App	Sequence 134, App	Sequence 132, App	Sequence 5, Appli	Sequence 11, Appl	Sequence 556, App	Sequence 100, App	Sequence 14, Appl	Sequence 1, Appli	ı,	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 92, Appl	Sequence 88, Appl	
	ID	US-10-616-101-2	US-09-972-115A-5	US-10-199-937-106	US-10-199-937-134	US-10-199-937-132	US-10-898-653-5	US-09-849-602-11	US-10-302-172-556	US-10-199-937-100	US-10-163-587A-14	US-10-199-937-1	US-10-616-101-1	US-09-972-115A-3	US-09-509-196A-1	US-09-972-115A-1	US-10-199-937-92	US-10-199-937-88	
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	Query Match Length DB	3816	4275	4406	4992	5002	6189	6018	5075	4127	5778	3508	3797	4297	3400	4493	2971	3353	
40	Query Match	100.0	99.4	99.4	99.4	99.4	99.4	99.3	98.8	94.2	94.0	91.8	88.9	87.6	86.4	79.6	63.9	63.9	
	Score	3816	3791.4	3791.4	3791.4	3791.4	3791.4	3788.4	3770.8	3595.8	3587.4	3504.8	3393.4	3341	3297	3039	2439.8	2439.8	
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Sequence 90, Appl Sequence 3, Appli Sequence 1, Appli Sequence 7, Appli Sequence 98, Appli	0 . 0	Sequence 40, Appl Sequence 177, Appl Sequence 177, App Sequence 159, App Sequence 947, App	Sequence 341, App Sequence 9472, Ap Sequence 45, App1 Sequence 104, App1 Sequence 10, App1 Sequence 2223, Ap	Sequence 5, Appli Sequence 11, Appl Sequence 9, Appli Sequence 17041, A Sequence 41, Appl
7 US-10-199-937-90 7 US-10-199-937-3 3 US-09-941-835-1 3 US-09-972-1158-7 7 US-10-199-937-98	7 US-10-252-157-342 3 US-09-641-835-7 10 US-10-898-653-4 3 US-09-841-835-9 8 US-10-276-774-340	3 US-10-994-8994-0 10 US-10-975-523-40 7 US-10-199-937-177 13 US-11-097-143-9473 7 US-10-199-937-138	7 US-10-252-157-341 13 US-11-097-143-9472 7 US-10-199-937-45 7 US-10-199-937-104 3 US-9972-1155-10 6 US-10-106-698-2223	7 US-10-199-937-5 7 US-10-181-447A-11 3 US-09-72-115A-9 3 US-09-918-955-17041 7 US-10-199-937-41 7 US-10-199-937-43
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ALIGNMENTS

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APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: As and Setty
APPLICANT: Haang, Betty
APPLICANT: Haang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
FILE REPRENCE: RIGL-010CIP3
CURRENT APPLICATION NUMBER: US/10/616,101
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 2000-10-425
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
CONTINUED OF THE CATION NUMBER: US 09/427,154
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
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100.0%; Score 3816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3816; Conservative 0; Mismatches
Sequence 2, Application US/10616101 Publication No. US20050074825A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Gerego Morin B.
APPLICANT: Malter. Funk D.
APPLICANT: Malter. Funk D.
TITLE OP INVENTION: A Second Mammalian Telomerase
TITLE OP INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT FILING DATE: 2001-10-05
PRIOR PLING DATE: 2000-41-10
PRIOR PLING DATE: 2000-04-10
PRIOR PLING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
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NAME/KEY: CDS
LOCATION: (284)..(3781)
COTHER INFORMATION:
US-09-972-115A-5
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ORGANISM: Homo sapiens
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2281 CAGCTGGTTATAATATAATTTAGAAGTTGCAGAGTATTTGTTACAACACGGAGCTGATGTGA 2340
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CCCTGGGCGGCGTCTTCCCGGGGGGCCTCGCCCTGCTGCGGGGCCCGGGGCTCCTGC TCCGGTTGCTGGCGGTGTTGCTGGCTG	961 TACCATTACACTGTCTTTATGGTCATTATGAGTAACTGAACTTTTGGTCAAGC 1020 1020 TACCATTACACATTGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTTGGTCAAGC 1079 1021 ATGGTGCCTGGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTT 1080 1080 ATGGTGCCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTT 1139 1081 CTAAGAACAGGGTTGAAATGCAATGGACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTT 1139 1141 CTAAGAACAGGGTTGAAGTACTTCTTTTTTTAAGTTATGGTGCAGACCCAACACTGC 1140 1141 TCAATTGTCACAATAAAAGTGCTATAGACTTCTCTTTAAGTTATGGTGCAGACCCAACACTGC 1199 1141 TCAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACACA

Db 3480 CCAAAAGCAATGTATATGGAATTGGAGTACTGGGTGTTCACAAAG 3539 Qy 3481 ACAGATCTTGTTACATTTGCCACAGGCAGCTACTGGGTACTGGGAAAGT 3540 Db 3540 ACAGATCTTGTTACATTTGCCACAGGCAGCTCTTTTGCCGGGTAACCTTGGGAAAGT 3599 Qy 3541 CTTTCCTGCAGTTCAGTGCAATGAAAATGGCACTTCTCCTCCAGGTCATCACTCAGTCA 3600 Db 3600 CTTCCTGCAGTTCAGTGCAATGAAAATGGCACTTCTCCTCCAGGTCATCACTCAGTCA 3659 Qy 3601 CTGGTAGGCCCAGTGCAATGAAAATGGCATTCTCCTCCAGGTCATCACTCAGTCA 3659 Qy 3601 CTGGTAGGCCCAGTGTAAATGGCATTAGCTGAATATTTACAGAGGAGAAC 3660 Db 3602 CTGGTAGGCCCAGTGTAAATGGCTTAGCTGAATATTTACAGAGGAGAAC 3719 Qy 3614 AGGCTTATCCTGAGTATTAATTACTTACCTGAATATTTACAGAGGAGAAC 3729 Qy 3621 AGGCTTATCCTGAGTATTTAATTACTTACCTGAATATTTACAGAGGAGAAC 3729 Qy 3721 GATAAATAGTTATTTAAGAACTAATTACCTGAAAATCATCAAAAGGTATGGTCGATG 3779 Qy 3721 GATAAATAGTTATTTAAGAAACTAATTCCACTAAAATCATCAAAAGGTATGGTCGATG 3739 Qy 3721 GATAAATAGTTATTTAAGAAACTAATTCCACTAAAATCATCAAAAGGTATGGTCGATG 3739 Qy 3721 GATAAATAGTTATTTAAGAAACTAATTCCACTAAAATCATCAAAAGGTATGGTCGATG 3739 Qy 3781 GCCTCTACGTTATTTTAAGAAAACTAATTCCACTAAAATCATCAAAAGCACGAGTG 3839 Qy 3781 GCCTCTACGTTTTTAAGAAAACTAATTCCACTGAAACTAAAAACACTCAAAAGCACTCAAAAGCACTCAAAACACTCAAAAACACTCAAAAACACTCAAAAACACTCAAAAACACTCAAAAACACTAAAAAA	RESULT 3 US-10-199-337-106 Sequence 106, Application US/1019937 Sequence 106, Deplication US/1019937 Publication No. US20030190739A1 GENERAL INFORMATION: APPLICANT: Christenson, Erik APPLICANT: DeMaggio, Anthony J. APPLICANT: Goldman, Phyllis S. APPLICANT: Modelligott, David L. TITLE OP INVENTION: TANKYRAEZ WATERIALS AND METHODS FILE REFERENCE: 27866/36559 CURRENT FILING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: US/09/606,035 PRIOR APPLICATION NUMBER: US/09/606,035 PRIOR PILING DATE: 1999-06-29 PRIOR PILING DATE: 2002 SEQ ID NO 106 LENGTH: 4406 TYPE: DAM ORGANISM: Homo sapiens PEATURE: FEATURE: FEATURE: NAME/KEY: CDS LOCATION: (2).(3787)	Query Match 99.4%; Score 3791.4; DB 7; Length 4406; Best Local Similarity 99.8%; Pred. No. 0; 1 Gaps 1; Gaps 1; Japs 1; Japs J
2341 ATGCCCAAGACAAAGGAGACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAG 2400 2400 ATGCCCAAGACAAAGGAGCATTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAG 2459 2401 ATGTAGCAGACAAAAGGAACTTATTCCTTTACATAATGCAGCATCTTACGGGCATGTAG 2459 2401 ATGTAGCAGCTCTACTAATAAAATAAATGCATGTCCAATGCCACGGACAAATGGGCTT 2460 2460 ATGTAGCAGCTCTACTAATAAAATAAATGCATGTTCAATGCCACGGACAAATGGGCTT 2519 2461 TCACACCTTTGCACGAAGCAGCCCAAAAGGAACAACACATTGTTGCTAG 2579 2520 CCACCGACGAAGCAGCCCAAAAGGAAGAACACACATTGTTGCTAG 2579 2521 CCCATGGAGCTGACCGACTCTTAAAAATCAGAAGAACACACATTGTTGCTTG 2579 2520 CCCATGGAGCTGACCGACTCTTAAAAATCAGAAGAACACAAACACTTTAGTTT 2639 2580 CCCATGGAGCTGACCGACTTTTGAAAAATCAGGAAGACCAAACACTTTAGTTT 2639 2581 CAGCGGATGATGTCAGCGCTTTTTGACAGGAAGGACCAAACACTTTAGTTT 2639 2640 GTTACAAGCCTCAACTGCTTCTGACAGCAGACCCATTGCTCTCTT 2699 2641 GTTACAAGCCTCAAGTGTGAGAAAGCCCAGGAGCCCATTGCTCTCT 7700 2700 GTTACAAGCCTCAATGGTGAGAAAGCCCAGGAGCCCATTGCAGATGCTCTCT 7759 2701 CTTCAAGGTCCAATGGTGTGAGAAAGCCCAGGAGCCACTGCAGATGCTCTTTTTTG 2710 2710 CTTCAAGGTCCAATGGTGTGAGAAAGCCTTTCTGCAGATGCTCTTTTTTTT	2761 GGAGTTTTCAGAACTGTCTCAGTAGTTAGTTCAAGTGGAACAGAGGTGCTTCCAGTT 2820 2820 GGAGTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTT 2879 2821 TGGAGAAAAAGGAGGTTCCAGGAGTTTAGTTAGTTCAAGTGGAACAGGAGGTGCTTCCAGTT 2879 2881 TGGAGAAAAAGGAGGTTCCAGGAGTAGTTTTAGCATACCAATTCGTAAGGATCTTG 2880 1	3181 GTGGAATCTTCAACAGATACTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTAT 3240 3240 GTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAACTAT 3299 3241 GGGAAAGATCTTCAACAATATTCTCAAGATTCTCAAGAGGTTTGTAACAACATTTTTTTT

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3052 ATGTAGCAGCTCTACTAATAAAGTATAATGCATGTCAATGCCACGGACAAATGGGCTT 3111 2461 TCACACCTTTGCACGAAGCGCCCAAAAGGGACGAACACAGCTTTGTGCTGCTG 2520	GGAGTITTCAGAACTGTCTTCAGTAGTTAGTTCAAGTGGAACAGGGGTGCTTCCAGTT [3181 GTGGAATCTTCAACAGATACTATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTAT 3240 3832 GTGGAATCTTCAACAGATATTCTCAAGATTCAGAAGGTTTGTAACAGAAACTAT 3891 3241 GGGAAAGATCACCCGGAGAAAAGAATTCTGAAGAAACCCACACACA

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Db 4202 CTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCA 4261 Qy 3601 CTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGTGTTATTACAGAGGAGAAC 3660 L	RESULT 6 US-10-898-653-5 Sequence 5, Application US/10898653 Sequence 5, Application WS/10898653 Sequence 5, Application WS/10898653 Septemblication No. US20050143370A1 GENERAL INFORMATION: TITLE OF INVENTION: Therapeutic Compounds TITLE OF INVENTION: Therapeutic Compounds CURRENT FILING DATE: 2004-07-23 CURRENT FILING DATE: 2004-07-23 SEQ ID NO 5 LENGTH: 6189 TYPE: DNA CORGANISM: Homo Sapien CORGANISM: Homo Sapien		421 CAGGITITIGGGGGAAAGACGTAGATATITIGTTCAGAATGGTGCAAATGTCCAG 48
	Qy 2761 GGAGTITTTCAGAACTGTCTTCAGTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTT 2820 Db 3422 GGAGTTTTTCAGAACTGTCTTCAGTAGTTCAAGTGGAACAGAGGTGCTTCCAGTT 3481 Qy 2821 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG 2880 Db 3482 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG 3541 Cy 2881 GACTTGAGCACTAATGATTATTGAGAGAACAAACACATTCGAAGGAATCTTTG 3541 Cy 2981 GACTTGAGCACCTAATGATATTTGAGAGAACAAACAGATCACTTTGGATGTATTAGTTG 3601 Cy 2941 AGATGGGCACAAGGAGCTGAAGGATTGGAATCAATTTGGATGTATTAGTTG 3601 Cy 2941 AGATGGGCACAAGGAGCTGAAGGATTGGAATCAATTATGGACATAGGCACAAAC 3000 Cy 2941 AGATGGGCACAAGGAGCTGAAGGAATTGGAATCATTATGGACATAGGCACAAAC 3661 Bb 3602 AGATGGGGCACAAGGAGTTGGAATTGGAATCATTATGGACATAGGCACAAAC 3661	3001 TARITAAAGGACTCGAGAGACTTATCTCCGGACAACAAGGTCTTAACCCATATTTAACTT 3060 3662 TAATTAAAAGGACTCGAGAGACATACTCGGACACAACAAGGTCTTAACCCATATTTAACTT 3721 3721 TGAACACCTCTGGTAGTGAGACAATTCTTATAGATCTGCTCTCTGATGATAAAGGGTTC 3781 3722 TGAACACCTCTGGTAGTGAACAATTCTTATAGATCTGCTCTCTGATGATAAAGGGTTC 3781 3722 TGAACACCTCTGGTAGTGAACAATTCTTATAGATCTGCTCTCTGATGATAAAGGGTTC 3781 3782 AGTCTGTGGAGAGAGACAATTCTTATAGATCTGCTCTCTCT	3481 ACAGATCTTGTTACATTTGCCACAGGCAGCTGTTTGCCGGGTAACCTTGGGAAAGT 3540

1716 TACAMACTIGCCOCCACTICGGGAATGAATGACACACCACTACACTICATACACCTICAGGGATTCT 1895
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Qy 3781 GCCTCTACGTTTTACTCCTTTGCTGAAAAAA 3813 Db 3936 GCCTCTACGTTTTACTCCTTTGCTGAAAAAA 3968	RESULT 7 US-09-849-602-11 Sequence 11, Application US/09849602 ; Publication No. US20030165834A1 ; GENERAL INFORMATION: ; APPLICANT: Scanlan, Matthew J. ; APPLICANT: Old, Lloyd J.	; APPLICANT: Stockert, Elisabeth ; APPLICANT: Chen, Yao-Tseng ; TITLE OF INVENTION: Colon Cancer Antigen Panel ; FILE REFERENCE: L0461/7105 (JRV) ; CURRENT APPLICATION NUMBER: US/09/849,602	; CURKENT FILING DATE: 2001-03-04 ; NUMBER OF SEQ ID NOS: 30 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 11 ; LENGTH: 6018 ; TYPE: DNA	3%; Score 3788.4; DB 3; Length 6018; 8%; Pred. No. 0;	Matches 3803; Conservative 0; Mismatches 6; Indels 1; Gaps 1; Qy 4 GCTGCTCGCCGCGGGGGCAGCCGAGGAGCCCAGCGAGGGGCGCGCGTG 63 Dy 1		Ay 124 TGAGCGCGTCTTCTCCGGGGGCCTCCTCCTCCTGGGGGGCGGGGGCTCCTGCTCC 183	Qy 184 GGTTGCTGGCGCTGTTGCTGGCTGGCGGCCGGCCGGTCGCGGTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCT	Qy 244 CCGGCGGGGGGGCCTGCGCCGGCCGGCCGAGGCCGTGGAGCCGGCCG	Oy 304 AGCTGTTCGAGGCGTGCCGCAACGGGACGTGGAACGAGTCAAGAGCTGGTGACGCCTG 363 300 AGCTGTTCGAGGCGTGCCGCAACGGGACGTGGAACGAGTCAAGAGGCTGGTGAGGCTTG 359	Qy 364 AGAAGGTGAAACAGCCGCGACACGGCGGCAGGAAATCCACCCCGCTGCACTTCGCCGCAG 423 1	Qy 424 GTTTTGGGCGGAAAGACGTTGTTGTTTTGCTTCAGAATGGTGCAAATGTCCAAGCAC 483 Db 420 GTTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAATGGTGCAAATGTCCAAGCAC 479	Qy 484 GTGATGATGAGGGGCCTTATTCCTCTTCATAATGCATGCTCTTTGGTCATGCTGAAGTAG 543	Qy 544 TCAAICTCCTTTTGCGACATGGTGCAGACCCCAAIGCTCGAGATAAITGGAATTATACTC 603	OY 604 CTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTACAGCATG 663
2701 CTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGCAGCCAGC	2761 GGAGTITITCAGAACTGTCTTCAGTAGTTCAAGTGGAACAGAGGGTGCTTCCAGTT 2820	GACTIGAGCACCTAAIGGATAITATITIGAGAGAACAGAICACTITIGGAIGIAITAGITIG	2941 AGAIGGGGCACAAAGAGCTGAAGAGGGATTGGAATCAATGCACATAGGCACAAAC 3000	3156 TAATTAAAGAGTCGAGAGACTTATCTCCGGACAAGGTCTTAACCCATATTAACTT 3215 3061 TGAACACCTCTGGTAGTAGAACAATTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTC 3120	3121 AGTCTGTGGAGGAAGATGCAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAG 3180 	3181 GTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACAAGAAACTAT 3240 	gogaaagatacactcaccgggaaaagaagtttctgaagaaaccacaaccatgccaatg 	AACGAATGCTATTCATGGGTCTCCTTTGTGAATGCAATTATCCACAAGGCTTTGATG 	AAAGGATGCGTACATAGGTGGTATGTTTGAGGTGGGATTTATTT	CCAAAACCAATCAATATGTATATGGAATTGGAGGGGGGGTCTGGGTGTCCAGTTCACAAG 	481 ACAGATCTTGTTACATTTGCCACAGGGGCTGCTTTTGCCGGGTAACCTTGGGAAAGT 	CTTTCCTGCAGTTCAGTGCAATGAAATGGCAATTCTCCTCCAGGTCATCAGTCA 	CTGGTAGGCCCAGTGTAAATGGCCTAGCATTAGGTGATATTTTACAGAGAGAACCCTGGTAACAGTGTAATTTACAGAGAGAG	AGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTGGTG	3/21 GAIAMATAGITATITAGAMACIMATICCACITAMACIMAMATAGAMAGAGAGAGG 3/80

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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Dramac, Radong J.
TITLE OF INVENTION: No. US20040053250Alel Arginine-rich Protein-like Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REPRESENCE: 803 LCNCP
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT APPLICATION NUMBER: US 10/225,251
PRIOR PILING DATE: 2002-08-20
PRIOR PELLING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt. FL_genes Version 2.0
SEQ ID NO 556
TENNAME: EACH
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APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: Goldman, Phyllis S.
TITLE OF INVENTION: TANKTRAEZ MATERIALS AND MET
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWAER: PALENTIN VEY: 2.0
SEQ ID NO 100
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                                                                                                                                          94.2%; Score 3595.8;
99.9%; Pred. No. 0;
vative 0; Mismatches
                                                                                                                                            Query Match
Best Local Similarity 99.99
Matches 3597; Conservative
                                       ; NAME/KEY: CDS
; LOCATION: (2)..(3508)
; FRATURE:
; NAME/KEY: 3'UTR
; LOCATION: (3509)..(4127)
US-10-199-937-100
TYPE: DNA
ORGANISM: Homo sapiens
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; Sequence 100, Application US/10199937; Publication No. US20030190739A1; GENERAL INFORMATION: APPLICANT: Christenson, Erik

RESULT 9 US-10-199-937-100

MAGITTICAL CACCTCTGGTAGTGGAACATTCTTATAGA 2880 MAGITTICAL CAGTCTGTGGAAGAAGAACTACAATTCG 3154 MAGITTICAL CAGTCTGTGGAAGAAGAACTACAATTCTTATAGA 2314 TCATGCAGGTGGAACAACAATACAATATTCTCAAGAT 3314 TCATGCAGGTGGAACAACAATACAATATTCTCAAGAT 3314 TCATGCAAGAACAACAACAACAATATTCATCGAAAAAAAA	US-10-163-587A-14	Query Match 94.0%; Score 3587.4; DB 6; Length 5778; Best Local Similarity 99.9%; Pred. No. 0; Matches 3588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 225 ATGTCGGGTCGCCGGTGCGCGGGGAAGCGGCTGCGCGGCGGCGGCGGCGGCGGCCGCGGCGCGCGGCG	Qy 285 GTGGAGCCGGCCCGAGAGCTGTTCGAGGCGTGCCGCAACGGGGACGTGGAGCGTC 344	QY 345 AAGAGGCTGGTGACGCAGGAAGGTGAACAGCCGCGACACGCGGGCAGGAAATCCACC 404 DD 121 AAGAGGCTGGTGATGAAGGTGAACAGCCGCGACACGGCGGGCAGGAAATCCACC 180	Qy 405 CCGCTGCACTTCGCCGCAGGTTTTGGCCGGAAAGACGTAGTTGAATATTTGCTTCAGAAT 464 Db 181 CCGCTGCACTTCGCCGCAGGTTTTGGCGGGAAAGACGTAGTTGAATATTTGCTTCAGAAT 240	Oy 465 GGTGCAAATGTCCAAGCACGTGATGAGGGGGCCTTATTCCTCTTCATAATGCATGC	Qy 525 TITGGTCATGCTGAAGTCAATCTCCTTTTGCGACATGGTGCAGCCCCAATGCTCGA 584 Db 301 TITGGTCATGCTGAAGTCAATCTCCTTTTGCGACATGGTGCAGCCCCAATGCTCGA 360	Qy 585 GATAATTGGAATTATACTCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGC 644	OY 645 ATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCA 704	Qy 705 TTGGATTTAGCAGATCCATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGA	Qy 765 CTCTTAGAAAGTGCCAGGAGTGGCAATGAAAAAAATGATGGCTCTACTCACCACTTA 824	Qy 825 AATGTCAACTGCCAGGCAAGTGATGGCAAAGTCAACTCCATTACATTTGGCAGCAGGA 884	Qy 885 TATAACAGAGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGCTAAA 944	Qy 945 GATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACT 1004	Qy 1005 GAACTTTTGGTCAAGCATGGTGCTGTGTAAATGCAATGGACTTGTGGCAATTCACTCCT 1064	OY 1065 CITCATGAGGCAGCTTCTAAGAACAGGGTTGAAGTATGTTCTCTTTAAGTTATGGT 1124	OY. 1125 GCAGACCCAACACTGCTCAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACCA 1184	Oy 1185 CAGTTAAAAGATTAGCATATGAATTTAAAGGCCACTCGTTGCAGGAGTGCACGA 1244
Db 2821 ACAAGGTCTTAACCCATATTAACT Oy 3095 TCTGTCTCCTGATGATAAAGAGTTTT 2881 TCTGTCTCCTGATGATAAAGAGTTTT Db 2941 AGAGCACAGAGTTGACAAGAACTA Oy 3215 TCGAAGGTTGTTAACAAGAACTA Oy 3215 TCGAAGGTTGTAACAAGAACTA Oy 3215 TCGAAGGTTGTAACAAGAACTA Oy 3215 TCGAAGAACACCATGCCAAT Oy 3315 TGCAATTATCCACAAAGCTTTGATA Oy 3315 TGCAATTATCCACAAAGCTTTGATA Oy 3315 TGCAATTATTTGCTGAAAACTCTTGATA Oy 3316 TGCAATTATTTTGCTGAAAACTCTTGATA Oy 3317 TGCAATTATTTTGCTGAAAACTCTTGATA Oy 3318 TGCAATTATTTTTGCTGAAAACTCTTGATA Oy 3311 TGCAATTATTTTTTTACAGAAACTCTTGATA Oy 3311 TGCAATTATTTTTTTACAGAAACTCTTGATA OY 3312 TGCAATTATTTTTACAGAAACTCTTGATA OY 3311 TCCCTCCAGGTCTCCAGTTCACAAA OY 3311 TCCCTCCAGGTCTCCAGTTCACAAA OY 3311 TTTTTACCGGGTAACTTTTACAGAGAAACTCT OY 3311 TCCTCTCCAGGTCACTCACTCACTCAAAA OY 3311 TTTTTACAGAGGAAAC OY 3311 TTTTTACAGAGGAAAA OY 3311 TATGAGGCTTATTTTACAGAGGAAAA OY 3311 TATGAGGCCTCAAAGAGTATGGTCGAT OY 3311 TATGAGGCCTCAAAGAGTATGGTCGAT OY 3311 TATGAGGCCTCAAAGGAAACGAGAAA OY 3311 TATGAGGCCTCAAAGGAAAGGAAACAGAAACAAAACAAA	ACAAGGICTTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTATAGA	TCTGTCTCCTGATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGGTGCAAGTACAGTTCG 	AGAGCACAGACATGGAGGTCATGCAGGTGGAATCTTCAACAGATACAATATTCTCAAGAT AGAGCACAGAGATGGAGGTCATGCAGGTGGAATCTTCAACAGATACATATCTCAAGAT	TCAGAAGGTTTGTAACAAGAAACTATGGGAAAGATACACTCACCGGAGAAAAGAAGTTTC 	TGAAGAAAACCACAACCATGCCAATGAACGAATGCTATTTCATGGGTCTCCTTTTGTGAA 	TGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGC 	TGGCATTTATTTTGCTGAAAACTCTTCCAAAAGCAATCAAT	aggtactgggtgtccagttcacaaagacagatcttgttacatttgccacaggcagctgct 	CTTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCACA 	TICTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAATGGCCTAGCATTAGC	IGAATATGITATTTACAGAGAGAACAGCCTTATCCTGAGTATTTAATTACTTAC	TATGAGGCCTGAAGGTATGGTCGATGGATAAATAGTTATTTTAAGAAACTAATTCCACTG	aacctaaaatcatcaaagcagcagtggcctctacgttttactcctttgctgaaaaaa 3 	87A-14		/RADIO SENSITI	PRIOR APPLICATION NUMBER: 60/296,110 PRIOR FILING DATE: 2001-06-07 NUMBER OF SEQ ID NOS: 40 SOFTWARE: Patentin version 3.1	EQ ID NO 14 EQ ID NO 14 TYPE: DNA ORGANISM: Homo sapiens	FEATURE: NAME/KEY: CDS LOCATION: (1)(3501) OTHER INFORMATION:

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                                                                              1003 TGGTGCCTGTGTAAATGCAATGAACTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTC
                                                                                                                       TAAGAACAGGGTTGAAGTATGTTCTCTTTAAGTTATGGTGCAGACCCAACACTGCT
                                                                                                                                                       1063 TAAGAACAGGGTTGAAGTATGTTCTCTTTTAAGTTATGGTGCAGACCCAACACTGCT
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                943 ACCATTACACAATGCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAGCA
                                                           1022 IGGIGCCIGIGIAAAIGCAAIGGACIIGIGGCAAIICACICCICIICAIGAGGCAGCIIC
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                                                                                   Sequence 1, Application US/10616101
; Publication No. US20050074825A1
; Publication No. US20050074825A1
; GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Huang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REFERENCE: RIGL-010CTP3
CURRENT APPLICATION NUMBER: US 09/643,159
PRIOR PILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR PILING DATE: 1999-10-25
PRIOR PLING DATE: 1999-10-25
PRIOR FILING DATE: 1999-10-25
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9
Matches 3394; Conservative
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; ORGANISM: Homo sapiens
US-10-616-101-1
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	643) Sequences not determined at this position . Unknown residue pul in to provide alignment. ture 680)	INFORMATION: Sequences not determined at this position . Unknown residue INFORMATION: in to provide alignment. KEY: misc feature ION: (682)(682)	; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put ; OTHER INFORMATION: in to provide alignment. ; NAME/KEY: misc feature ; NAME/KEY: misc feature	<pre> ; LOCATION: (711)(713) ; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put ; OTHER INFORMATION: in to provide alignment. ; NAME/KEY: misc_feature ; .TOTANTON: (1971) ; TOTANTON: (1971) </pre>	FORMATIO FORMATIO : misc f	. \\\ \cdots\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\) OTHER INFORMATION: Sequences not determined at this position . Unknown residue put ; OTHER INFORMATION: in to provide alignment. ; NAMEKEY: misc feature ; NAMEKEY: misc feature	<pre>p. DOCATION: (2180)(1880) p. THER INFORMATION: Sequences not determined at this position . Unknown residue put profile INFORMATION: in to provide alignment. p. NAME/KEY: misc. feature. p. NAME/KEY: misc. feature.</pre>	<pre>i. LOCATION: (2209)(2505) i. THER INFORMATION: Sequences not determined at this position . Unknown residue put i. OTHER INFORMATION: in to provide alignment. i. NAME/KEY: misc. feature. i. NAME/KEY: misc. feature.</pre>	<pre>; LOCATION: (2221)(2221) ; OTHER INFORMATION: Sequences not determined at this position . Unknown residue put ; OTHER INFORMATION: in to provide alignment. ; NAME/KEY: misc feature</pre>	<u>೧೯೮೮</u>	<pre> // DOCATION: (2316)(5316) // OTHER INFORMATION: Sequences not determined at this position . Unknown residue put // OTHER INFORMATION: in to provide alignment. // NAME/KEY: misc_feature // NAME/KEY: misc_feature // NAME/KEY: misc_feature // DOCATION: In the provide alignment is not become a sequence of the provide alignment. // NAME/KEY: misc_feature // NAME/KEY: misc_</pre>	CONTER INFORMATION: (2359)(46744) COTHER INFORMATION: Sequences not determined at this position . Unknown residue put COTHER INFORMATION: in to provide alignment. NAMEKEY: misc feature COMMITTON: (2077) (2077)	ORMATION ORMATION misc_fe	(227)(227) NRMATION: Sequences not de NRMATION: in to provide al	Query Match 87.6%; Score 3341; DB 3; Length 4297; Best Local Similarity 89.0%; Pred. No. 0; Matches 3400; Conservative 8; Mismatches 402; Indels 12; Gaps 2;	Oy 1 CGCGCTGCTCCGCCGCGGGGGCAGCCGGGGGGGGGGGGG	OY 61 TGGGCGCGGCCCATGGGCCGGATCCGGTGACAGCAGGAGCCAAGCGGCCCGGG 120 Db 134 GTGGCGCGGCCATGGGACTGCGCCGGTGACAGCAGGAGGAGCCAAGCGGCCCGGG 193
	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put	Unknown residue put
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TYPE: DNA ORGANISM: Homo sapiens

FEATURE:

LOCATION: (1)..(3999) OTHER INFORMATION: NAME/KEY: CDS

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TITLE OF INVENTION: A Second Mammalian Telomerase FILE OF INVENTION: A Second Mammalian Telomerase FILE OF INVENTION: A Second Mammalian Telomerase; PILE OF INVENTION: 0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/0.001/
                                                       2401 ATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTGAGTGGGGCACAAGGAGCTG 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAATTCTTATAGAACTGTCTCCTGATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATG 2640
                                                                                                                                                                                      CTTATCTCCGGACAACAAGGTCTTAACCCATATTTAACTTTTGAACACCTCTGGTAGTGGA 3080
                                                                                                                                                                                                                                                                                                                         CTTATCTCCGGACAACAAGGTCTTAAACCCATATTAAACTTTGAACACCTCTGGTAGTGGA 2580
                                                                                                                                                                                                                                                                                                                                                                                                                   ACAATTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATG 3140
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                                                                                                                                                       AAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGAGAGA 3020
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (626)...(626)
OTHER INFORMATION: Sequences not determined at this position. Unk.
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (629)...(629)
OTHER INFORMATION: Sequences not determined at this position. Unk.
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (638)...(638)
OTHER INFORMATION: Sequences not determined at this position. Unk.
OTHER INFORMATION: Sequences not determined at this position. Unk.
LOCATION: (691)...(694)
OTHER INFORMATION: Sequences not determined at this position. Unk.
NAME/KEY: misc_feature
LOCATION: (691)...(694)
OTHER INFORMATION: Sequences not determined at this position. Unk.
NAME/KEY: Misc_feature
LOCATION: (691)...(694)
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OTHER INFORMATION: Sequences not determined at this position .
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (1)...(586)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc_feature
LOCATION: (596)...(597)
OTHER INFORMATION: Sequences not determined at this position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (724)..(724)
OTHER INFORMATION: Sequences not determined at this position
OTHER INFORMATION: in to provide alignment.
NAME/KEY: misc feature
LOCATION: (730)..(730)
                                                                                                                                                                            OTHER INFORMATION: Sequences not determined at this position OTHER INFORMATION: in to provide alignment.

INAME/KEY: misc feature
LOCATION: (621)..(621)
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Sequences not determined at this position OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc feature
LOCATION: (626). (626)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Sequences not determined at this position OTHER INFORMATION: in to provide alignment.

NAME/KEY: misc feature
LOCATION: (764)...(764).
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NAME/KEY: misc feature
LOCATION: (7917..(791)
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NAME/KEY: misc. feature
LOCATION: (2148). (2148).
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NAME/KEY: misc feature
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LOCATION: (2382)..(238)
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Sequence 1, Application US/09972115A Publication No US20030032769A1 GRNERAL INFORMATION: APPLICANT: Greog, Morin B. APPLICANT: Greog, Morin B. APPLICANT: Walter, Funk D.

	937 ATGCTAAAGATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTCATTATG 996	997 AAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAAATGCAATGGACTTGTGGCAAT 1056 1247 AAGTAACTGAACTTTTGGTCAAGCATGGCTGCTGTGTAAATGCAATGGACTTGTGGCAAT 1306	1057 TCACTCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTTGAAGTATGTTCTTCTTTA 1116	1117 GTTATGGTGCAGACCCAACACTGCTCAATTGTCACAATAAAAGTGCTATAGACTTGGCTC 1176	1177 CCACACCACAGFITAAAGAAGATTAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAG 1236 	1237 CTGCACGAGAAGCTGATGCTCGAATCAAAAACATCTCTCTGGAAATGGTGAATT 1296 1487 CTGCACGAGAAGCTGATGTTACTCGAATCAAAAAACATCTCTCTC	1297 TCAAGCATCCTCAAACACATGAAACAGCATTGCATTGTGCTGCTGCTTCCATATCCCA 1356	aagaaagcaaatatgtgaactgttgctaagaaaggagcaaacatcaatgaaaggcta 			1537 ACAGAGCTGCATATTGTGGTCATCTACAAACCTGCCGCTACTCCTGAGCTATGGGTGTG 1596	1597 ATCCTAACATTATATCCCTTCAGGCCTTTACTGCTTTACAGATGGGAAATGAAATGTAC 1656 	1657 AGCAACTCCTCCAAGAGGGTATCTCATTAGGTAATTCAGAGGCAGACAATTGCTGG 1716	1717 AAGCTGCAAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCA 1776 	1777 ACTGCAGAGACATTGAAGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGTATAACA 1836 		1897 GAGGCCTIGTACCTTIGGACAATGCATGTTCTTATGGACATTATGAGGTTGCAGAACTTC 1956 2147 GAGGCCTTGTACCTTTGCACAATGCATGTTATGGACATTATGAAGTTGCAGAACTTC 2206 2157 TTGTTAAACATGCACATGCATGTTTATGGACATTATGAAGTTGCAGAACTTC 2206 1957 TTGTTAAACATGCAGTAGTTAATGTTATGGAAATTTACACCTTTACATG 2016
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OTHER INFORMATION: Sequences not determined at this position . Unknown residue put OTHER INFORMATION: in to provide alignment.	LOCATION: (2398) (2398) CONTROL OF THE TOTAL OF THE TOTAL OF THE INFORMATION: Sequences not determined at this position . Unknown residue put OTHER INFORMATION in to provide alignment.		DCATION: (2468)(2468)	LOCATION: (2493) (2493) OTHER INFORMATION: Sequences not determined at this position . Unknown residue put OTHER INFORMATION: in to provide alignment.	NAME AND THE TEST OF THE PROPERTY OF THE POSITION . Unknown residue put OTHER INFORMATION: Sequences not determined at this position . Unknown residue put OTHER INFORMATION: A CONTRACT IN TO PROVIDE Alignment.	LOCATION: (3163)	NAMICAL: MADEL LEGUITE LOCATION: (3488)(3498) OTHER INFORMATION: Sequences not determined at this position . Unknown residue put OTHER INFORMATION: in to provide alignment.	uery Match 79.6%; Score 3039; DB 3; Length 4493; est Local Similarity 88.5%; Pred. No. 0; atches 3101; Conservative 1; Mismatches 375; Indels 27; Gaps 2;	gagtcaagaggtggtgacgcctgagaaggtgaacagcggggacacggggg 	397 AATCCACCCGGTGCACTTCGCCGCAGGTTTTGGGCGGAAAAGGTAGTTGATTTGC 456	ATAATG	CATGCTCTTTTGGTCATGCTGAAGTAGTCAATCTCCTTTTGCGACATGGTGCAGACCCCA	ATGCTCGAGATAATTGGAATTATACTCCTCCCATGAAGCTGCAATTAAAGGAAAGATTG	ATGITTGCGATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAA	GGACACATTGATTTAGCAATCCATCTGCCAAGCAGTGCTTACTGGTAATAAGA	AGATGAACTCTTAGAAGTGCCAGGAGTGCAATGAAGAAAAATGATGGCTCTACTCA	CACCATTAAATGTCAACTGCCACGCAAGTGATGGCAGAAAGTCAACTCCATTACATTTGG

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Oy 3091 TAGATCTGTCTCCTGATGATAAAGAGTTTCAGT Db 3347 TAGATCTGTCTCTGATGATAAAGAGTTTCAGT OY 3151 TTCGAGAGCACAGAGATTGAGGTCATGCAGGTC OY 3211 AGATTCAGAAGGTTTGTAACAAGAACTATG- Db 3467 AGATTCAGAAGGTTTGTAACAAGAACTATG- Db 3467 AGATTCAGAAGGTTTGTAACAAGAACTATG- DD 3467 AGATTCAGAAGGTTTGTAACAAGAAACTATG-	3250 3327 3310 3370 3370	Oy 3430 ATCAATATGTATATGGAATTGGAGAGGTACTCTTTTTTTT	Oy 3610 CCGGTGTAAATGGCCTAGCATTAGCTGAATATG Db 3887 CCGGTGTAAATGGCCTAGCATTAGCTGAATATIII Db 3870 CTGAGTATTAATTACTTACCAGATTATGGGGG Oy 3730 TTATTTAAGAACTAATTCCACTGAACTAAA Oy 3730 TTATTTAAGAACTAATTCCACTGAACCTAAA Oy 3790 TTATTTAAGAACTAATTCCACTGAACCTAAA Oy 3790 TTTACTCCTTTGCTGAAAAAAA 3813 Db 4067 TTTTACTCCTTTGCTGAAAAAAA 4990	Search completed: December 18, 2006, 21:40:51 Job time : 3883.64 secs	
TTGTTAAACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATG AGCAGCAGCAGAAAAGGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACC	2387 ATATTCAAGATNTGCTTAGGGGAGATGCAGTTTTGTTAGATGCTGCCAAGAAGGGTTGTT 2446 2197 TAGCCAGAGTGAAGATTGTCTTCTCCTGATAATTGCCGCGATACCCAAGGCA 2256 [2371 TACATAATGCAGCATCTTACGGGCATGTAGATGTAGAGCTCTACTAATAAAGTATAATG 2430 2627 NANNANANANANANANANANANANANANANANANANAN	2551 AGGAAGGACAAACACTTTAGATTTAGTTTCAGCGGATGATGTCAGCGCTCTTCTGACAG 2610 2807 INNINININININININININININININININININI	GTTCAAGTGGAACAGAGGTGCTTCCAGTTTGAGAAAAAGGAGGTTCCAGGAGTAGATT [2971 GAATCAATGCTTATGGACATAGGCACAAACTAAAGGAGTCGAGAGACTTATCTCCG 3030

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           3430 ATCAATATGTATATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTT
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**EMC Celerra SIDS3/ptodata/1/pubpna/USO6_NEW_PUB.seq:**

**EMC Celerra SIDS3/ptodata/1/pubpna/USO6_NEW_PUB.seq:**

**EMC Celerra SIDS3/ptodata/1/pubpna/USO8_NEW_PUB.seq:**

**EMC Celerra SIDS3/ptodata/1/pubpna/PCT NEW_PUB.seq:**

**EMC Celerra SIDS3/ptodata/1/pubpna/USI0_NEW_PUB.seq:**

**EMC Celerra SIDS3/ptodata/1/pubpna/USI1_NEW_PUB.seq:**

**EMC Celerra SID
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286109,
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                                                                                                                                                December 18, 2006, 17:00:26; Search time 757.887 Seconds
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-266-748A-251004
US-11-266-748A-99554
US-11-266-748A-99554
US-11-266-748A-152365
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US-11-266-748A-165504
US-11-266-748A-244089
US-11-266-748A-116071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              3026960 seqs, 1061187768 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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3816
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Match Length
                       Copyright
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                                                                                  GENERALI INFORMATION:

APPLICANT: JOHNSton, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Methods of Using the Same
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2005-01-14
PRIOR PELING DATE: 2005-07-18
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0; Mismatches
Sequence 23750, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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US-11-266-748A-23750
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Best Local Simi:
Matches 3806;
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1296 TCAATTGTCACAATAAAAGTGCTATAGACTTGGCTCCCACACCACAGTTAAAAGAAAG	1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC 1260 	1261 GAATCAAAAACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAA 1320 	1321 CAGCATTGCATTGTGCTGCATCTCCATATCCCAAAGGAAAGAAA	1181 TGCTAAGAAAAGGAGCAAACATCAATGAAAAGACTAAAGAATTCTTGACTCCTCTGCACG 1440 	1441 TGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGTGGTGAAACATGAAGCAAAGG 1500 	1501 TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATC 1560 	1561 TACAAACCTGCCGCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG 1620 	1621 GCTTTACTGCTTTACAGATGGGAAATGAAAAGTACAGCAACTCCTCCAAGAGGGTATCT 1680 	1681 CATTAGGTAATTCAGAGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCG 1740 	1741 AAACTGTAAAAAACTGTGTGTGTCGAGTGTCAACTGCAGAGACATTGAAGGGCGTC 1800 	1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAATATCTGC 1860 	1861 TACAGCATGGAGCTGATGTGCTAAAGATAAAGGGGCCTTGTACCTTTGCACAATG 1920 	1921 CATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA 1980 	1981 ATCTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATG 2040 4	2041 AAATTTGGAAACTTCTGCTCCAGGAFGGTGCAGACCCTACCAAAAAAAAAGGATGGAA 2100 	2101 ATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAG 2160 	2161 ATGCAGCTTTGCTAGATGCTGCCAAGAAGGCTTTAGCCAGAGTGAAGAAGTTGTCTT 2220 2316 ATGCAGCTTTGCTAGATGCTGCCAAGAAGGCTTGTTTAGCCAGAGTGAAGAAGTTGTTT 2375 2221 CTCCTGATAATGCTGCCGCGATACCCAAGGCAGAGTCAAGACCTTTAGATTAGC 2280
61 TGGGCGGGCCCATGGGACTGCGCGATCCGGTGACAGCAGCCAAGCGGCCCGGG 120		1 TCCGGTTGCTGGCGCTGTTGCTGGCGGCGGGGGGCGGGGGG	1 CCCCCGGGGGGGGGCGGCGGGGGGGGGGGGGGGGGGG	01 GAGAGTIGTTCGAGGCGTGCCCCAACGGGACGTGGAACGAGTCAAGAGCTGGTGACGCGGGGGGGG	1 CTGAGAAGGTGAACAGCCGCGACACGGCGGCCAGGAAATCCACCCCGGTGCACTTCGCCC	1 CAGGITITIGGGCGAAAACGTAGTTGAATATTTGCTTCAGAATGGTGCAAATGTCCCAG	1 CACGIGATGAGGGGCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAG	TAGTCAATCTCCTTTTGCGACATGGTGCAGATGCTCGAGGTAATTGGAATTATA	TAGICANICICITITISCOATITAAAGAAAGTITGATGTTTGCATATATITATA CTCCTCTCCATGAAGCAATTAAAGAAAGATTGATGTTTGCATTGGTGTTTACAGC	ATGGGGCCACCACCATCCGAAATACAGATGGAAGGACAGCTTGGCTTGGCGCGCTACACCCTACACCCACC	CATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGA	GRAGGGGGGATGAAAAAAGGGGGGGGGGGGGGGGGGGGG	GONGIGGCARLORAGARARATORIGGGICIACIACACACATIARATORICACACACAGATACATACATTAGGAGGAGAGATATAACAGAGGAGAGAGA	1 ITGTACAGCTGTTACTGCAACATGGAGCTGATGTTTGGCAACATATAACAGTAAAGATTACAGAACATGGATCTGG		ATGGTGCCTGTGTAAATGCAATGGGCTTGTGGGCATTCACTCCTCTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGCAGCTTTCATGAGAGCAGCTTTCATGAGAGCAGCTTTCATGAGAGCAGCTTTCATGAGAGAGA	114 114 129 120

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0y 3361 AAAGGCATGCGTACATAGGTGGTATTTGGAGCTGGCATTTATTT	RESULT 2 US-11-266-748A-23602 US-11-266-748A-23602 Sequence 23600, Application US/11266748A PUBLIcation No. US20060134663A1 GENERAL INCORMATION PREPLICANT: MAILSHAM, Rav1 TITLE OF INVENTION: Methods of Using the Same FILE REPRENCE: 55815-010 (319189) CURRENT PAPLICATION NUMBER: US/11/266,748A CURRENT PAPLICATION NUMBER: B04105479.2 PRIOR PLILING DATE: 2004-11-03 PRIOR PLILING DATE: 2005-07-18 PRIOR PLILING DATE: 2005-07-18 PRIOR PLILING DATE: 2005-07-18 PRIOR PLILING DATE: 2005-07-18 PRIOR PLILON DATE: 2005-07-18 PRIOR P
2316 CTCCTGATAATTGCGGGATACCCAAGGCAGACATTCAACACCTTTACATTTAG 2435 2281 CAGCTGGTTATAATAATTTAGAAGTTGCAGAGTATTGTTACAACACGGGGCTGATGTG 2340 [11	2761 GGAGTTTTTCAGAACTGTTCAGTAGTTCAAGTGGAACAGGGGGGCTTCCAGTT 2820 2916 GGAGTTTTTCAGAACTGTTCAGTAGTTAGTTCAAGTGGAACAGGGGGCTTCCAGTT 2915 2917 GGAGAAAAAGGGGTTCCAGGAGTTAGTTCAAGTGGAACAGGGGGGTGCTTCCAGTT 2915 2821 TGGAGAAAAAGGAGTTCCAGGAGTAGTTTTTAGCATAACTCAATTCGTAAGGAATCTTG 2880 2918 GACTTGAGCACCTAATGGATAATTTTGAGAGAACAGATCCATTCGTAAGGAATCTTG 2035 2881 GACTTGAGCACCTAATGGATAATTTTGAGAGAACAGATCCATTTGGTATGTTG 2910 3036 GACTTGAGCACCTAATGGATAATTTTGAGAGAACAGATCCATTTTGATTG 2095 3041 AGATGGGGCACAAGGAGTTAATTTTGAGAGAACAATCAAT

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Oy 1166 AGACTTC Db 1081 AGACTTC OY 1226 GTTGCTC Db 1141 GTTGCTC OY 1286 AATGGTC Db 1201 AATGGTG	Oy 1346 TCCATAI Db 1261 TCCATAI OY 1406 TGAAAAC OY 1466 TGAAAAC OY 1466 TGAAAAC OY 1526 GACTTCT Db 1381 TGTTGTI Db 1381 TGTTGTI Db 1381 TGTTGTI	Oy 1586 CTATGGG Db 1501 CTATGGG OY 1646 TGAAAAI Db 1561 TGAAAAI OY 1706 ACAATTG Db 1621 ACAATTG OY 1766 TCAGAGI	1681 1826 1741 1880 1801 1946 1951 2006	1981 2126 2041 2186 2101
Matches 3726; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 86 GGATCCGGTGACAGCGAGCCCAGGCCCTGAGCGCTTTTCTCCGGGGGG 145 Image: Conservation of the conservation of		420 565 480 625 540 685	660 805 720 865 780 925 840	986 TGGTCATTATGAAGTAACTTATGGTCAAGCATGGTCTGTGTAAATGCAATGGA 1045 901 TGGTCATTATGAAGTAACTTTTGGTCAAGCATGGTGCTGTGTAAATGCAATGGA 1045 1046 CTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTTGAATGTTGTTC 1105 961 CTTGTGGCAATTCACTCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTTGAAGTAGTTC 1105 1106 CTTGTGCCAATTCACTCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTTGAAGTTGTTC 1020 1107 TCTTCTCTTAAGTTATGGTGCAACACTGCTCAATTGTCAAATAAAAGTGCTAT 1165 1081 TCTTCTCTTAAGTTATGGTGCAACACTGCTCAATTGTCAAATAAAAGTGCTAT 1080
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	RESULT 3 US-11-266-748A-29428 US-11-266-748A-29428 Sequence 29428, Application US/11266748A Publication No. US20060134663A1 GENERAL INPORMATION: APPLICANT: Harkin, Paul APPLICANT: Johnson, Patrick APPLICANT: Mulligan, Karl TITLE OF INVENTION Transcriptome Microarray Technology and TITLE OF INVENTION WHORE: US/11/266,748A CURRENT PELICATION NUMBER: ED 01103 FILE REFERENCE: 5818-10.02 (319189) CURRENT PELICATION NUMBER: ED 04105482.6 PRIOR FILING DATE: 2004-11-03 PRIOR PELING DATE: 2005-03-14 PRIOR PELING DATE: 20
1216 TACCCAAGGCAGACATTCAACACCTTTACATTTAGCAGCTGGTTATAATATTTAGAAGT 2305 1	2786 AGTTAGTTCAAGTGGAACAGAGGTCTTCCAGTTTGGAGAAAAAGGAGGTTCCAGGAGT 2160 2846 AGATTTTAGCATACTCAATTCGTAAGGAATTTGGAGAAAAAGGAGGTTCCAGGAGT 2760 2846 AGATTTTAGCATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATGGATATAT 2905 2906 TGACAGACACACATCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATGGATATAT 2905 2906 TGACAGACACACATCAATTCGTAAGGAATCTTGGACTTGAGCACCTAATGGATATAT 2905 2906 TGACAGACACACACATTTGATTCAGTTGAATTGAGCACCTAATGGATATAT 2905 2910 TGACAGACACACACACATTTGAATTCAGACTCAATTAAAGGAGTCTAATGGATATAT 3025 2821 TGACAGACACACACACATACGCACAAACTAATTAAAGGAGTCCAAGGACTTAT 3025 2821 TGACAGACACACACACACATACACATTTAAACTTTGAACACACTTTATAAGAGACTTAT 3025 2841 GATTGGAATCAATTGACATTAAGATTTAAACTTTGAACACCTTGAGGACTTAT 3025 2841 GATTGGAATCAATGACTTAAGCCAAAACTAATTAAAGGAGTCGAAGACATAT 3005 2906 GATTGGAAACAACAACATTAAGCACAAACTTTAAAGAGAGTCGAAGAACATT 3005 2906 TCCCGACAACAACAACATTAAACTTTGAACACTTTTAAAGAGAGTCGAAGACATTA 3025 2911 [

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COCGANISM: Homo Sapiens
US-11-266-748A-22929
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2607 AAGGGTGGTTTAATTCCTCTTCATAATGCGGCATCTTATGGGCATGTTGACATAGCGGCT 2666
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US-11-266-748A-100.

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 58815-0102 (139189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR PELING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PRILICATION NUMBER: EP 04105485.9
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US-11-266-748A-251004
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
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17.4%; Score 663.8; DB 8; Length 99.0%; Pred. No. 1.3e-151; rative 0; Mismatches 7; Indels
    Query Match
Best Local Similarity 99.03
Matches 668; Conservative
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APPLICANT: MUNITI, FAGIL
APPLICANT: MUNITION. Patrick
APPLICANT: MUNITION. Rari
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methode of Using the Same
FILE REPERENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-18
NUMBER OF SEQ ID NOS: 493996
SOFTWARE PREACTIN VERSION 3.3
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99.7%; Pred. No. 8.9e-129;
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Best Local Similarity 99.7°
Matches 592; Conservative
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p ORGANISM: Homo Sapien8
US-11-266-748A-99554
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LENGTH: 594
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APPLICANT: HORANTION:
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2005-01-10-03
PRIOR PELING DATE: 2005-01-10-03
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-07-18
NUMBER OF SEC ID NOS: 483996
SEC ID NO 311521
LENGTHREET
PRIOR PELING DATE: 2005-07-18
NUMBER OF SEC ID NOS: 483996
SEC ID NO 311521
LENGTHREET
PRIOR DATE: 2015-07-18
NUMBER OF SEC ID NOS: 483996
SEC ID NO 311521
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                                                                                                                                                        Sequence 311521, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
CTGTCTCCTGATGAT 3110
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; ORGANISM: Homo Sapiens
US-11-266-748A-311521
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TGAATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTG 180
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APPLICANT: Harrin, Paul
APPLICANT: Harrin, Paul
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 152365
LENGTH: 594
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14.9%; Score 570; DB 8; L
Best Local Similarity 99.7%; Pred. No. 8.9e-129;
Matches 592; Conservative 0; Mismatches 0;
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Sequence 152365, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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CORGANISM: Homo Sapiens
US-11-266-748A-152365
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3213 ATTCAGAAGGTTTGTAACAAG-AAACTATGGGAAAGATACACTCACCGG-AGAAAGAAG 3270

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3451 GAGGAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGC 3510
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354. GAGGAGGTACTGGGGGTGTCCAGTTCACAAAGACAGATCTTGTTACTATTTGCCACAGGCAGC
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US-11-266-748A-189602
US-11-266-748A-189602
US-11-266-748A-189602

Sequence 189602, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPRENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105492.6

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

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PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2005-01-14

PRIOR PILING DATE: 2005-01-14

PRIOR PILING DATE: 2005-01-18

PRIOR PILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PatentIn version 3.3

SEQ ID NO 189602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 AACACGTGTGTAAATGCAACAGATAAGTGGGCGTTTACTCCCCCCCTCCATGAAGCAGCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                        1887 AAAGATAAAGGAGGCCTTGTACCTTTGCACAATGCATGTTCTTATGGACATTATGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AAGGGCTGCCTGGCAAGAGTGCAGAAGCTCTGTACCCCCAGAGAATATCAACTGCAGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 Acccaggecagaarricaaccccrcrecaccreecagecageraraaraaccreeaagra
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                                                                                                                                                        1707 CAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTATGTT
                                                                                                                                                                                                 12 CGACTCTTAGAGGCATCTAAAGCTGGAGACTTGGAAACTGTGAAGCAACTTTGCAGCTCT
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                                                                      Length 929;
                                                                                                             Indela
                                                               Query Match 14.0%; Score 535.6; DB 8; Best Local Similarity 74.0%; Pred. No. 2.8e-120; Matches 679; Conservative 0; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2607 ACAGCAGCCATGCCCCCA 2624
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; ORGANISM: Homo Sapiens
US-11-266-748A-189602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                      GENERAL INFORMATION:

APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITIE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT FILING DATE: 2005-11-03
PRIOR PELING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 0410549.2
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2005-01-14
PRIOR PELING DATE: 2005-01-18
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-18
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Pred. No. 6.5e-120;
0; Mismatches 4;
US-11-266-748A-55144
; Sequence 55144, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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Best Local Similarity 99.3%;
Matches 536; Conservative (
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                                                                                                                                                            3754 GAACCTAAAATCATCAAAGCAGCAGTGGCCTCTACGTTTTACTCCTTTGCTGAAAAAAA
                                                                                                                                                                                      3694 TTATGAGGCCTGAAGGTATGGTCGATGGATAAATAGTTATTTAAGAAACTAATTCCACT
                                                                       1723 CAAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTGTCAGAGTGTCAACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586 CAAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hartin, Paul
APPLICANT: Hartin, Paul
APPLICANT: Muligan, Rari
APPLICANTON: Transcriptome Microarray Technology and
TITLE OF INVENTION: Wethods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PELLING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELLING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 165504, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION: APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEX: misc feature
LOCATION: (220). (228)
OTHER INFORMATION: n is a, c, g, or t
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                US-11-266-748A-165504/c
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   CTACGITITACTCCTTTGCTGAAAAAA 3813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3334 ATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATTTGGAG 3393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCAC 3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3574 ATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAATGGCCTAGCATTAG 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGTACTGGGTGTCCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGCTGC 240
                                          61 ATGCAATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTTTGCCGGGTAACCTTGGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAATGGCAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIGAATATGITATITACAGAGGAGAACAGGCITAICCIGAGIATITAATIACITACCAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGAAGAAAACCACAACCATGCCATTGAACTAATGCTATTTCATGGGTCTCCTTTTGTGA 60
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                                                                                                                            RESULT 11
US-11-266-748A-217436
Sequence 217436, Application US/11266748A
PUBLication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: MINISTON: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION: MCHBRE: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT PILING DATE: 2004-11-03
PRIOR PLING DATE: 2005-01-18
PRIOR PLING DATE: 2005-01-18
PRIOR PLING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 564;
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Pred. No. 6.5e-120;
0; Mismatches 4;
3754 GAACCTAAAATCATCAAAGCAGCAGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.3%;
Matches 536; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-266-748A-217436
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                                                                                                                                                                                                                                                                                                                                                                                                                  1963 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAG 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 CAGCCAAAGGAAAATTTGAAATTTGCAACTTCTGCTCCAGCATGGTGCAGACCCTACNN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 NNNNNNCAGGGATGGAATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTC 502
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143 GAGACATTGAAGGGCGTCAGTCTACACCCCTTCATTTTGCAGCTGGGTATAACAGAGTGT
                                                                                                                  CCGTGGTGGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCAAAAGGAAAATATGAAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTACCA
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                                                                                                                                                                                   203 ccercercantarcrecracacarcacrearererecarecranadaranaeaecc
                                                                                                                                                                                                                                                                                                              263 TIGTACCTITIGCACAATGCATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAG
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TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58819-1002 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
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Pred. No. 2.3e-112;
0; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-266-748A-116071
; Sequence 116071, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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Best Local Similarity 76.2
Matches 619; Conservative
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                                                                                                                                                                                                                          2023 CAGCAAAAGGAAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTACCA 2082
                                                                                                                                                                                                                                                                                                                                                                           2083 AAAAAACGGGATGGAAATACTCCTTTGGATCTTGATAAAGATGGAGATACAGATATTC 2142
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                                                                            1963 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAG 2022
                                                                                                                                                 346 AACATGGAGCAGTAGTTAATGTAGCTGATTTTATGGAAATTTTACACCTTTACATGAAGCAG 287
                                                                                                                                                                                                                                                                    286 CAGCCAAAGGAAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTACNN 227
                                                                                                                                                                                                                                                                                                                                                                                                                     226 NNNNNNCAGGGATGGAAATACTCCTTTGGATCTTGTTAAAGATGGAGATACAGATATTC 167
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406 TIGIACCTITGCACAATGCATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTA 347
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US-II-226-748A-244089
Publication No. US20060134663A1
Sequence 244089, Application US/11266748A
Publication No. US20060134663A1
Sequence 244089
Rublication No. US20060134663A1
Sequence 244087
Sequence 244089
Full CANT: Multigan, Ratl
APPLICANT: Multigan, Ratl
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: WHORER: US/11/266,748A
CURRENT FILING DATE: 2006-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2005-01-14
PRIOR PELING DATE: 2005-01-14
PRIOR PELING DATE: 2005-01-18
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 244089
FENTILE FOR PERIOR PERIOR PERIOR PELING DATE: 2005-07-18
PRIOR PELING DATE: 2005-07-18
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13.5%; Score 515.6; DB 8; Length 668;
Best Local Similarity 97.6%; Pred. No. 1.7e-115;
Matches 518; Conservative 0; Mismatches 13; Indels 0
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LOCATION: (441)...(449)
OTHER INFORMATION: n is a, c, g, or t
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US-11-266-748A-244089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3557 IGCAATGAAAATGGCACATTCTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGT 3616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1617 AAATGGCCTAGCATTAGCTGAATATGTTATTTACAGAGGAGAACAGGCTTATCCTGAGTA 3676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578 TGGTTCTCTTTCATTAATGCCATTATTCATAAAGGGTTTGATGAGCGACATGCATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518 AGGAGGAATGTTTGGGGCCGGGATTTATTTTGCTGAAAACTCCTCAAAAAGCAACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3437 TGTATATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACAŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3497 ITGCCACAGGCAGCTGCTCTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAG
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Pred. No. 2.3e-112;
0; Mismatches 193;
                 PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2006-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PALCHIN VERSION 3.3
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.2%;
Best Local Similarity 76.2%;
Matches 619; Conservative
  FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
US-11-266-748A-158235
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2957 GCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGA 3016
                             GTTGAAAGAAATAGGCATCAATGCATATGGGCCACCGCCACAAATTAATCAAAGGAGTAGA 122
                                                                                                                       AAGACTCTTAGGTGGACAACAAGGCACCAATCCTTATTTGACTTTTCACTGTGTTAATCA 182
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; Sequence 158235, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION; Baul
APPLICANT: HARKIN, Paul
APPLICANT: Mulligan, Karl
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Techn
; TITLE OF INVENTION: Methods of Using the Same
; FILE REPRERNCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT PILING DATE: 2005-11-03
; PRIOR PAPLICATION NUMBER: EP 04105492.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR PILING DATE: 2004-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR APPLICATION NUMBER: EP 04105507.0
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Wed Dec 20 07:34:47 2006

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Search completed: December 18, 2006, 19:31:42 Job time : 762.887 secs

Human tan Human Grb Human SPA Human col Human tan

AAY72589 AAY05734 AAB47022

Human tan Human tan

Aay 72589 Aay 05734 Aay 05734 Aab 27209 Aab 27209 Aab 27210 Aab 27210 Aab 27210 Aab 62286 Aab 6286 Aab 6286 Aab 66896

AAU79537 ADR14791 AAB27210 AAB47023 AAB48574 AAB66285

5556 5676 5776

Human

Amino aci Human tan

Human tan Mouse SPA Human bre Human tan Human tan Drosophil

Protein o Human tru

Truncated Human tan

Aau79539 Ady97768 1 Aao20512

AAU79539 ADY97768

AA020512

AAB66286 ABB60894 AAB66297 AAY44404 AL I GNMENTS

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                Copyright
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- protein search, using sw model OM protein December 18, 2006, 17:21:00; Search time 139.536 Seconds (without alignments) 3489.682 Million cell updates/sec Run on:

US-10-616-101-3

Title: Perfect score:

5585 1 GFGRKDVVEYLLQNGASVQA.....AMKWAHSPPGHHSVTGRPSV 1065 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 segs, 457216429 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genese(m1)980s:* genese(m2)00s:* genese(m2)00s:* genese(m2)001s:* genese(m2)003s:* genese(m2)003as:* geneseqp2004s:* geneseqp2005s:* A_Geneseq_8:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:

SUMMARIES

Ady97761 Human tan Ady97770 Human tan Ady97730 Human tan Asy9748 Tankyrase Abg73732 Tankyrase Abg73730 Tankyrase Ady97766 Human tan Ady66295 Human tan Ady66295 Human tan Ady66286 Human tan Ady66288 Human tan Ady66288 Human tan Ady66299 Human tan Ady697767 Human tan Ady97762 Human tan Ady97762 Human tan Ady97762 Human tan Ady97762 Human tan ABP69457 ADR14792 AAB66288 ADY97766 AAB66295 ABG73730 ADH69405 AAY97749 Length DB 1169 1240 1240 1240 1240 1262 1287 1287 1385 1100 Query Match Score Result

Tankyrase Human tan

Human Human Human

Adr66429 Adr66087 Aab66294 Abg73735 Ady97769

AAB66294 ABG73735 ADY97769

ADR66087

ADY97762 AAB66290 ADR66429

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control with a control; (2) treating (M1) an individual with a cell cycle related disorder, which involves administering to the individual an inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I), comprising a nucleic acid that hybridizes under high stringent conditions to a sequence complementary to the 3797 base pair sequence of ADY97759 or the 3816 base pair sequence of ADY97759 or ADY97760; (II) comprising (II) operably linked to regulatory sequences recognized by a host cell (IV) transformed with the nucleic acid (5) a host cell comprising (II) of producing (I); (7) a polypeptide that specifically binds to (I); and (8) inhibiting (M2) growth of a tumor of cell, involves contexting the tumor with a bloactive agent capable of inhibiting TaHo activity. (I) is useful for screening a bloactive agent capable of modulating (I), or screening for agents capable of interfering inhibiting growth of a tumor cell by a bloactive agent capable of individual with a cell cycle related disorder. (M2) is useful for inhibiting growth of a tumor cell by a bloactive agent e.g. antisense collowing in a tumor cell by a bloactive agent e.g. antisense collowing in a tumor cell by a bloactive agent e.g. antisense collowing in a proper cell cycle related disorder. (M2) is useful for human tankyrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologue isotype 1.
             &$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 1065 AA;

ô Gaps ; 0 DB 9; Length 1065; Indels ö 100.0%; Score 5585; 100.0%; Pred. No. 0; tive 0; Mismatches Query Match
Best Local Similarity 100.
Matches 1065; Conservative

9 1 GFGRKDVVEYLLONGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT ઠે

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ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360 ALHCADAS PYPKRKQI CELLLRKGANI NEKTKEFLTPLHVAS EKAHNDVVEVVVKHEAKV 301 301 420 420 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNI I SLQGFTALQMGNENVQQLLQEGIS NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 361 361

PDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLI PLHNAASYGHVD 601 601

VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS

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1020 1020 900 096 900 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE RSCYICHROLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065 781 196 1021 841 901 901 961 781 셤 임 셤 g ઠે ò ð ઠ ઠે

Human tankyrase homologue isotype 1 mutant protein SEQ ID NO:12 Z ADY97770 standard; protein; 1083 (first entry) 16-JUN-2005 ADY97770; RESULT 2 ADY97770

cell cycle; cancer; cytostatic; tankyrase homologue isotype 1; mutein. 08-JUL-2003; 2003US-00616101 US2005074825-A1. sapiens. 07-APR-2005 Synthetic. Homo

25-OCT-1999; 99US-00427154 25-OCT-2000; 2000US-00696668 25-APR-2001; 2001US-00843159. OSSOVSKAYA V. HUANG B. CHAN E. LUO Y. (CHAN/) (XUXX/) (HUAN/) 1 (LUOY/)

tankyrabe e.g. protein cycle Novel recombinant polypeptide such as cell o homolog, useful for screening its modulator.

Оввоувкауа V;

Huang B,

Chan E, Xu X,

Luo Y,

540

WPI; 2005-294737/30

Disclosure; SEQ ID NO 12; 75pp; English.

600 999 9 720 720

The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (TaHo). Comprising an amino acid sequence having 85% or more acquence identity to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described (I) diagnosing cancer, which involves determining the activity of (I) from a test sample of an individual and comparing the level with a control with a control; (2) treating (MI) an individual with a cell cycle

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inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I); comprising a nucleic acid that hybridizes under high stringent conditions to a sequence complementary to the 3797 base pair sequence of ADY97759 or the 3816 base pair sequence of ADY97759 or ance sequence identity to ADY97760, or a nucleic acid having 85% or more sequence identity to ADY97759 or ADY97760; (4) an expression vector (III) comprising (II) operably linked to requising exceptions are comprising (II) or (III); (6) producing (I); (7) a polypeptide that comprising (II) or (III); (6) producing (I); (7) a polypeptide that comprising (II) or (III); (6) producing (I); (7) a polypeptide that comprising (II) or (III); (6) producing (II); (7) a polypeptide that comprising (II) or (III); (8) producing (II); (9) a bloactive agent capable of inhibiting TaHo activity. (I) is useful for screening a bloactive agent capable of inhibiting of (I), or screening for agents capable of interfering with the binding of (I), or screening for agents capable of individual with a cell cycle related disorder. (M2) is useful for individual with a cell cycle related disorder. (M2) is useful for contacting prowth of a tumor cell by a bloactive agent e.g. antisense be appresent sequence represents a human tankyrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologue isotype 1 mutant protein
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Sequence 1083 AA;

420 540 600 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360 301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 480 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540 541 ICKLLLOHGADPTKKONRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720 1 GFGRKDVVEYLLGNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60 SGNEEKOMALLTPLINVNCHASDGRKSTPLHLAAGYNRVKIVOLLLOHGADVHAKDKGDLV 241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 0; Gaps DB 9; Length 1083; 0; Indels Query Match 100.0%; Score 5585; Best Local Similarity 100.0%; Pred. No. 0; Matches 1065; Conservative 0; Mismatches 601 61 481 181 181 241 421 541 601 661 121 301 361 421 g 셤 ò 8 셤 ò 유 Š g ò 셤 ò g Š

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<i>≿</i> 8	781 SFSELS 	SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840
<i>8</i>		
č	901 SVEEEN	OSTVREHENDGGHANGTIFNRYNILKIOKVCNKKLWERYTHRRKEVSEENHNHANE 960
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ò t	961 RMLFHC	RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
3 &		
3		RSCYICHRQLLFCRYTLGRSFLQFSAMMAHSPEGHHSVTGRPSV 1065
RESULT ABG7373 ID AB	DT 3 73736 ABG73736 standard	ırd; protein; 1084 AA.
¥ ¥	ABG73736;	
X E	-APR-2003	(first entry)
X 8	пкугаве Н	isotype 1 TH-1 variant Taho E/A dC.
X & X	nkyrase; tostatic;	tankyrase H; cell cycle protein; growth inhibitor; TH-1; TaHo; immunostimulant; gene therapy; vaccine; cancer; tumour;
X X 8	il cycle	рогу
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PH PT	y gion	
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F F	gion	
FT	noip	/label= Ankyrin_repeat_3 89113
F. F.	noin	/label= Ankyrin_repeat_4
. F. F.	grom. 8c-difference	/label= Ankyrin_repeat_5
	nion	/note= "TH1 start" 147 176
	aio:	/label= Ankyrin_repeat_6
H		
FF	gion	210241 /label= Ankyrin_repeat_8
F. F.	gion	243281 /label= Ankyrin_repeat_9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a tumour cell. The methods are useful for screening for a bloactive agent capable of binding to a cell cycle protein tankyrase H, or a bloactive gent capable of modulating a cell cycle protein tankyrase H or PARP (poly ADP-tibose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents the tankyrase H isoform 1, Taho E/A C, which contains a Cal to Ala mutation and has a truncated C-terminal containing a 2 amino acid insertion described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                      is mutated from Glu (wild type, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid encoding a cell cycle protein, useful diagnosing and treating a cell cycle related disorder, e.g. cancer.
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/label= Ankyrin_repeat_19
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797. .845
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Ankyrin_repeat_15
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956. .1084
/label= PARP_domain
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ABG73732) to Ala"
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Matches 1065; Conservative
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AAY97748 standard; protein; 1100 AAY97748 RESULT

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1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT

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AAY97748

PLHBAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120

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301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV
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                                                                                                                                                                                                                                                                                                                                     Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer.
                                                   Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation; cell cycle protein; cell cycle associated disorder; cancer; gene mapping; chromosome mapping; gene therapy; vaccine.
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                          Tankyrase homologue isotype 1 protein sequence
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cive 0; Mismatches
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06-AUG-2001 (first entry)
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Best Local Similarity 100.
Matches 1065; Conservative
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                                                                                                        Unidentified.
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                                                                                                 361 NALDNIGGISLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
                                                                                                                                                               LGNSEADRÒLLEAAKAGDVETVKKLCTVQSVNCRD I EGRQSTPLHFAAGYNRVSVVEYLL
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301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV
                                                                   361 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
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243. .281
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283. .332
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/label= Ankyrin_repeat_2
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/label= Ankyrin_repeat_6
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/label= PARP_domain
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invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a tumour cell. The methods are useful for screening for a bioactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or pare (poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents tankyrase H isoform 1, TH-1, described in the
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                                                              RMLFHGSPFVNAITHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
                                                                        RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
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                                                                                                                                                                                                                         Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-1; TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour; cell cycle related disorder; poly ADP-ribose polymerase; PARP.
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       SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE
MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ
                               SVEEEMQSTVREHRDGGHAGGI PNRYNILKI QKVCNKKLWERYTHRRKEVSEENHNHANE
                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid encoding a cell cycle protein, useful diagnosing and treating a cell cycle related disorder, e.g. cancer.
                                                                                                        RSCYICHROLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065
                                                                                                                                                                                                                                                                                                                                                             Chan E, Xu X, Huang B, Ossovskaya V;
                                                                                                                                                                                                          Tankyrase H isotype 1 TaHo-1.from clone TH-1.
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                                                                                                                                                          ABG73730 standard; protein; 1100
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                                                                                                                                                                                                                                                                                                                                             (RIGE-) RIGEL PHARM INC.
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N-PSDB; ABQ77066.
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This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant acitivity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of tumour cell. The methods are useful for screening for a bioactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or PARP (poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents the tankyrase H isoform 1, TaHo-1, isolated from clone TH-1 which is described in the disclosure of the invention

Sequence 1100 AA;

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  DB 6; Length 1100;
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Query Match 100.0%; Score 5585; Best Local Similarity 100.0%; Pred. No. 0; Matches 1065; Conservative 0; Mismatches
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1020 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020 960 120 120 180 240 300 300 360 360 420 420 480 480 540 540 600 900 99 99 720 720 780 780 840 840 900 900 180 9 9 241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET PDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD SPSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE SVBEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT PLHEAAIKGKIDVCIVLLOHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 301 ALHCAAASPYPKRKQICELLIRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV IGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 541 ICKLILLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS SFSBLSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE SVEBEMOSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI VQLLLQHGADVHAKDKGDLV ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 361 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQBGIS LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 541 ICKLILQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLI PLHNAASYGHVD VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL RSCYICHROLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065 421 Н 121 781 1021 61 121 181 241 301 421 481 481 601 601 661 721 781 901 901 961 961 유 용 à 8 셤 ò g ò

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ADDVSALLITAAMPPSALPSCYKPQVINGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
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                                      NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
                                                  LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL
                                                                                                   QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
                                                                                                                                                                                                                                    PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
                                                                                                                                                                                                                                                                                   VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
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                                                                                                                                                                                                                                                                                                                                                                                    Screening for a bioactive agent capable of interfering with the binding of a tankyrase H cell cycle protein and p21 for diagnosing or treating cancer by combining a tankyrase H cell cycle protein, a candidate bioactive agent and p21.
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bioactive agent screening; cancer; cytostatic; human.
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                                                                                                                                                                                                                                                                                     protein e.g. tankyrase homologue (Tatho), comprising an amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (1) diagnosing cancer, which involves determining the activity of (1) from a test sample of an individual and comparing the level with a cell control with a control; (2) treating (M1) an individual with a cell cycle related disorder, which involves determining the level with a cell cycle related disorder, which involves administering to the individual an inhibitor of Tatho; (3) a recombinant nucleic acid (11) encoding (1), comprising a nucleic acid that hybridizes under high stringent conditions to a sequence complementary to the 379 base pair sequence of ADY97769 or the 3816 base pair sequence of ADY97760, (4) an expression vector (11) comprising (11) operably linked to regulatory sequences recognized by a host cell (1V) transformed with the nucleic acid; (5) a host cell comprising (11) operably linked to regulatory sequence call (1V) transformed with the nucleic acid; (5) a host cell comprising (11) or (11); (6) producing (17); (7) a polypeptide that expression of cell, involves contacting the tumor with a bioactive agent capable of inhibiting Tatho activity. (1) is useful for screening a boactive agent capable of individual with a cell cycle related disorder. (M2) is useful for individual with a cell cycle related disorder. (M2) is useful for call, involves individual with a cell by a bioactive agent e.g. antisense the human tankyrase become activity.
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                                                                                                                                         Ossovskaya V;
                                                                                                                                                                                                  Novel recombinant polypeptide such as cell on homolog, useful for screening its modulator.
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                        Huang B,
25-OCT-2000; 2000US-00696668.
25-APR-2001; 2001US-00843159.
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HUANG B.
OSSOVSKAYA V.
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(XUXX/)
(HUAN/)
(OSSO/)
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361 NALDNIGOTSIHRAAYCGHLOTCRILLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
                         361 NALDNIGGTSLHRAAYGGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQGGIS
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inflammatory disorder.
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Claim 9; SEQ ID NO 1504; 1012pp + Sequence Listing; English
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                                                                                                                                                The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different verations, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telemere-specific binding protein. The regulation of telemere length, in which TRF1 has a role, is all linked to against and cancer. The sequences are useful in the treatment of cancers and inflammatory
                                                                                                                                                                                                                                                                                                                            09
                                                                            New tankyrase2 polypeptides, useful for treating conditions mediated by poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders.
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                       Goldman PS, Mcelligott
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                                                                                                                            Claim 3; Page 200-203; 242pp; English
                       Demaggio AJ,
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Matches 1064, Conservative
                                            2001-102896/11
(ICOS-) ICOS CORP
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                     Christenson E,
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1027 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCFVHKD 1086
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847 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE
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                                                                                                     ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao QA, F
Ghosh M;
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Ma Y, Yamazaki V, Chen R, Wang Z,
J, Wang D, Drmanac RT;
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nucleotide sequence selected from any of 948 sequences (17 complements) and nucleotide sequence selected from any of 948 sequences (18211119).

AB212066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polymucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Ablaheimer's diseases), autoimmune diseases (multiple sclerosis, placeter or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 0;
1; Mismatches 0; Indels 0
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Best Local Similarity 99.9%;
Matches 1064; Conservative 1
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SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a candidate adenomatous polyposis coli protein (APC) and axin pathways modulating agent for treating cancer by contacting an assay system comprising a modifier of APC and axin polypeptide or nucleic acid
787 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
                           RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD
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11.FEB-2003; 2003US-044738P.
10-APR-2003; 2003US-0461789P.
14-MAY-2003; 2003US-0479650P.
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modulating agent. The method is useful in identifying a candidate adenomatous polyposis coil protein (APC) and a pathways modulating agent which are useful for sparing a composition for diagnosing or treating cancer. The present sequence represents a human orthologue of a Cancer. Accordabolitis elegans MAPCAX polypeptide. The sequence was identified
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tive 1; Mismatches
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Best Local Similarity 99.9
Matches 1064; Conservative
                                                                    using BLAST analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory
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poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
inflammatory and autoimmune disorders.
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Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;

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iive 1; Mismatches
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                                                                                                                         28-JUN-2000; 2000WO-US017827
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Human tankyrase2 related protein sequence SEQ ID NO:

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           PDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
                                                                                                                                                          VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
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QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
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This sequence is the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-2 protein. The TaHo proteins are useful for inducing or preventing cell proliferation. The TaHo cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the genetic disorders. The TaHo and for the genetic analysis of individuals with genetic disorders. The TaHo proteins, and their coding sequences are
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Novel recombinant cell cycle polypeptide, tankyrase H useful for inducir or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer.
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661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

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Best Local Similarity 99.9
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                                                                                                                                                                                                                                                                                                                                                                                            Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2; TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour; cell cycle related disorder; poly ADP-ribose polymerase; PARP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of tumour cell. The methods are useful for askyrase H, or a bioactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or PARP
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                                                                                                                                                                                                                                       RSCYICHROLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSV 1065
                                                                                                                                                                                                                                                                                                                                                                       Pankyrase H isotype 2 TaHo-2 fragment from clone K23
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(poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents the tankyrase H isoform 2, TaHo-2, isolated from clone K23 which is described in the disclosure of the invention
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US-10-199-937-99	US-10-276-774-1690	US-09-841-835-8	US-10-199-937-160	US-10-199-937-178	US-10-616-101-9	US-10-055-877-140	US-10-450-763-31331	US-10-756-149-4917	US-10-821-234-1120	US-10-450-763-37734	US-10-055-877-141	US-10-205-194-117	US-10-108-260A-3237	US-10-450-763-52303	US-11-097-143-1776	US-11-097-143-29028	US-10-055-877-139
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ALIGNMENTS

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APPLICANT: Chan, Eva APPLICANT: Chan, Eva APPLICANT: Chan, Eva APPLICANT: Hang, Betty APPLICANT: Hang, Betty Standy, Betty Hand, Betty Hand, Betty Hand, Betty Hand, Betty Standy Betty Standy Hand, Waleria TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods CURENT FILE REPREBRIES: RIGH-OUGLTP3 CURRENT APPLICATION NUMBER: US/10/616,101 CURRENT APPLICATION NUMBER: US/09/843,159 PRIOR FILING DATE: 2001-04-25 PRIOR APPLICATION NUMBER: US 09/696,668 PRIOR FILING DATE: 2000-10-25 PRIOR PRILING DATE: 1999-10-25 PRIOR PILING DATE: 1999-10-25 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin version 3.1 SEQ ID NO 3 TENERMY 10.5
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Best Local Similarity 100.0%; Pred. No. 0;
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Sequence 3, Application US/10616101 Publication No. US20050074825A1 GENERAL INFORMATION: 
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100.0%; Score 5585;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches
    09/427,154
                                                                                                                            CTHER INFORMATION: synthetic mutant US-10-616-101-12
PRIOR APPLICATION NUMBER: US 09/
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 1083
                                                                                     TYPE: PRT ORGANISM: Artificial sequence
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APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Huang, Betty
APPLICANT: Huang, Betty
APPLICANT: Huang, Betty
APPLICANT: Huang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REPRENCE: RIGH-010CIP3
CURRENT APPLICATION NUMBER: US 09/843,159
PRIOR PILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/696,668
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    NCHNKSA I DLA PTPQLKERLAYEFKGHSLLQAAREADVTR I KKHLSLEMVNFKHPQTHET
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US-10-616-101-12
US-10-616-101-12
; Sequence 12, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
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Sequence 6, Application US/09972115A
Sequence 6, Application US/09072115A
Seneral Invention
APPLICANT Geron Corporation
APPLICANT Geron Corporation
APPLICANT Geron Marie B.
APPLICANT Wideczyslaw, Platyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/033C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Version 3.1
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CRGANISM: Homo sapiens
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Sequence 8. Application US/10616101

GENERAL INFORMATION:

APPLICANT: Luo, Ying

APPLICANT: Chan, Eva

APPLICANT: Xu, Xiang

APPLICANT: Xu, Xiang

APPLICANT: AL, Missing

APPLICANT: AL, Missing

APPLICANT: Nu, Xiang

APPLICANT: Nu, Xiang

APPLICANT: Nu, Xiang

APPLICANT: Ossovskaya, Valeria

APPLICANT: Ossovskaya, Valeria

TITLE OF INVENTION TAIMYTARSE H, Compositions Involved in the Cell Cycle and Methods

TITLE OF INVENTION TAIMYTARSE H, Compositions Involved in the Cell Cycle and Methods

FILE REFERENCE: RIGL-010CIP3

CURRENT APPLICATION NUMBER: US 09/643,159

PRIOR PPLING DATE: 2000-10-25

PRIOR APPLICATION NUMBER: US 09/656,668

PRIOR PPLING DATE: 2000-10-25

PRIOR PPLING DATE: 1999-10-25

NUMBER OF SEQ ID NOS: 19

SEQ ID NOS: 19

SEQ ID NOS: 19

SEQ ID NOS: 19
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Sequence 15, Application US/10163587A
Publication No. US20030096263A1
Publication No. US20030096263A1
GENERAL INFORMATION:
APPLICANT: Oliveira, Marcos
TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
FILE REFERENCE: 50229-306
CURRENT APPLICATION UNMBER: US/10/163,587A
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/296,110
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTI OF VERSION 3.1
SEQ ID NO 15
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Sequence 2, Application UB/1019937

Sequence 2, Application UB/1019937

Publication No. US20010470739A1

SEMEDAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: Coldman, Phyllis S.
APPLICANT: Goldman, Phyllis S.
TITLE OF INVENTION: TANKTRASEZ MATERIALS AND METHODS
TITLE OF INVENTION: TANKTRASEZ MATERIALS AND CURRENT APPLICATION NUMBER: US/10/199,937

CURRENT APPLICATION NUMBER: US/09/606,035

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/141,582
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Sequence 135, Application US/10199937
Publication No. US20030190739A1
SERRAL INFORMATION:
APPLICANT: Christenson, Erik
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RESULT 8
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                                                                                                         Query Match 99.9%; Score 5582; DB 4; Length 1169; Best Local Similarity 99.9%; Pred. No. 0; Matches 1064; Conservative 1; Mismatches 0; Indels 0
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: PatentIn Ver. 2.0
                                  SEO ID NO 2
LENGTH: 1169
TYPE: PRT
ORGANISM: Homo sapiens
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970 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1029 1030 RMLFHGSPFVVAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1089 ö 120 549 240 309 489 129 300 369 429 361 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480 9 190 SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 250 PLHNACSYGHYEVTELLVÆHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIBGRQSTPLHFAAGYNRVSVVEYLL 901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 70 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR SGNEERMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL .; 0 4; Length 1169; 1021 RSCYICHROLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSV 1065 Sequence 101, Application US/10199937
| Sequence 101, Application US/20630190739A1
| JERNERAL INFORMATEON:
| APPLICANT: Demaggio, Anthony J. APPLICANT: Goldman, Phyllis S. APPLICANT: Goldman, Phyllis S. APPLICANT: McElligott, David L. TITLE OP INVENTION: TANKTRASE2 WATERIALS AND WETHODS FILE REFERENCE: 27866/36559
| CURRENT FILING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: US/09/606,035 |
| PRIOR APPLICATION NUMBER: Go/141,582 |
| PRIOR APPLICATION NUMBER: 60/141,582 |
| PRIOR APPLICATION NUMBER: 60/141,582 |
| PRIOR PLING DATE: 1999-06-29 |
| WUMBER OF SEQ ID NOS: 178 .. 0 Query Match 99.9%; Score 5582; DB Best Local Similarity 99.9%; Pred. No. 0; Matches 1064; Conservative 1; Mismatches SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 101 TYPE: PRT ORGANISM: Homo sapiens

1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60	61 PLHEAAIKGKIDVCIVLLQHGABPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120 	121 SGNEEK-MALLIPLAVVACHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180	181 PLHNACSYGHYEVTELLUVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240	241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEWVNFKHPQTHET 300	301 ALHCAAASPYPKRKQICELLIRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360	361 NALDNIGGISLHRAAVGHLOTCRLLLSYGCDPNIISLGGFTALQMGNENVQQLLQEGIS 420	421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 	481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLMKFTPLHEAAAKGKYE 540	541 ICKLILQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600	601 PDNVNCRDTGGRHSTPLHLAAGYNNLEVAEXLLQHGADVNAQDKGGLIPLHNAASYGHVD 660	661	721 ADDVSALLTAAMPFSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780	781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFBREQITLDVLVE 84 	841 MGHKELKEIGINAY 	901	961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020	1021 RSCYICHROLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
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OY 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540 	QY 541 ICKLLIQHGADPTKRNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600 	QY 601 PDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660 	Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGFTQLCALLLAHGADPTLKNQEGGTPLDLVS 720 	OY 721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSISAASSLDNLSG 780 	Qy 781 SFSELSSYVSSSGTEGASSLEKKEVPGVDFSITQFYRNLGLEHLMDIFEREQITLDVLVE 840	Oy 841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900 	CY 901 SVBEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960	Qy 961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020 Db 1030 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1089	Qy 1021 RSCYICHRQLLFCRVTLGKSFLQPSAMKMAHSPPGHHSVTGRPSV 1065 	RESULT 9 US-10-616-101-4	; Sequence 4, Application US/IU616101 ; Publication No. US2050074825A1 ; GENERAL INFORMATION: ; APPLICANT: Luo, Ying		; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods; FILE REFERENCE: RIGL-010CIP3; CURRENT APPLICATION WUMBER: US/10/616,101; CURRENT FILING DATE: 2003-07-08	; PRIOR APPLICATION NUMBER: US 09/843,159 ; PRIOR FILING DATE: 2001-04-25 ; PRIOR APPLICATION NUMBER: US 09/696,668 ; PRIOR FILING DATE: 2000-10-25		; SEQ ID NO 4 ; LENGTH: 1240 ; TYPE: PRT ; ORGANISM: Homo sapiens	<pre>US-10-616-101-4 Query Match Best Local Similarity 99.9%; Score 5582; DB 5; Length 1240; Best Local Similarity 99.9%; Pred. No. 0; Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;</pre>

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                 Sequence 107, Application US/10199937
Publication No. US20030190799A1
SENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-199-937-107
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661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
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gequence 133, Application up/10199937

publication No. US200301907391

GENERAL INFORMATION.

APPLICANT: Christenson, Erik

APPLICANT: Goldman, Phyllis S.

APPLICANT: Goldman, Phyllis S.

TITLE OF INVENTION: TANKTRASE MATERIALS AND METHODS

FILE REFERENCE: 27866/36559

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US/09/606,035

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 178

SEQ ID NO 133

LENGTHAR: PATERIAL VOR: 2.0

LENGTHAR: PATERIAL VOR: 2.0
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PRIOR APPLICATION NUMBER: US 09/843,135
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR PILING DATE: 2000-10-25
PRIOR PILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic mutant US-10-616-101-11
                                                                                                                                                                                     ORGANISM: Artificial sequence
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Best Local Simi]
Matches 1064; (
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Publication No. US20050074825A1
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Xu, Xiang
APPLICANT: Will and APPLICANT: And APPLICANT: Will applicate the Compositions Involved in the Cell Cycle and Methods
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REPRENCE: RIGH-010CIPS
CURRENT APPLICATION NUMBER: US/10/616,101
CURRENT FILING DATE: 2003-07-08
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US-10-616-101-11
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US-09-849-602-26

Squence 26, Application US/09849602

Publication No. US20030155834A1

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Chen, Yao-Teng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105(URV)
CURRENT APPLICATION NUMBER: US/09/849,602

CURRENT FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 30

SOFFWARE: Patentin version 3.0
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US-09-849-602-26
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LENGTH: 1227
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Patent No. US2002037582A1

Patent No. US2002037582A1

Patent No. US2002037582A1

PAPLICENT. BOGGT. D. BOGGT. U.

TITLE OF INVENTION: Proteins

TITLE OF INVENTION: Proteins

TITLE OF INVENTION: Proteins

FILE REFERENCE: 1871-129

CURRENT APPLICATION NUMBER: US/09/509,196A

CURRENT FILING DATE: 1997-09-23

PRIOR FILING DATE: 1997-09-23

PRIOR PRING DATE: 1998-09-23

PRIOR PLING DATE: 1998-09-23

PRIOR PLING DATE: 1998-09-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver: 2.1

SECTION OF SEQ ID NOS: 2

SOFTWARE: PARCENTIN OF SEQ ID NOS: 2

SOFTWARE: PATENTIN OF SEQ ID NOS: 2
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                                                                      MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
                                                                                                                    SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960
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Best Local Similarity 99.5%;
Matches 1034; Conservative
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ORGANISM: Homo sapiens
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EVABLLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLV
                  481 EVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLV
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
Sequence 2, Application US/09841835
Sequence 2, Application US/09841835
Fatent NO. US20020076795A1
GENERAL INFORMATION:
APPLICANT: General, Sean
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCES ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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82.7%; Pred. No. 0;
tive 97; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230
TELECOMMUNICATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/841,835 FILING DATE: CLASSIFICATION: PRIOR PELICATION DATA: PROLICATION NUMBER: 09/196,387
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                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.7%
Matches 882; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                      SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180
                                                                                                                                                                                                   SGNEEKAMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 308
                                                                                                                                                                                                                                                    PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
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                                                                                                                                                                                                                                                                                                                                                               428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

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          LENCTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-3
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APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Huang, Betty
APPLICANT: Huang, Betty
APPLICANT: Ossovakaya, Valeria
TITLE OF INVENTION: TANKTAREH, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS
TITLE REFERENCE: A-68292-1/RAS/DHP
CURRENT APPLICATION NUMBER: US/09/696,668
CURRENT APPLICATION NUMBER: US/09/696,668
CURRENT APPLICATION NUMBER: US/09/427,154
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 11
SOFFWARE: Patentin version 3.1
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Patent No. 6617102
GENERAL INFORMATION:
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Sequence 6, Application US/09972115A
Sequence 6, Application US/09972115A
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Malter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR PELING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
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Patent No. 688765

GENERAL INFORMATION:
APPLICANT: Luo, Yin
APPLICANT: Luo, Yin
APPLICANT: Chan, Evan
APPLICANT: A, Xiang
APPLIC
                                                     RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
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iive 0; Mismatches
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Best Local Similarity 100.
Matches 1065; Conservative
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; ORGANISM: Homo sapiens
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US-09-843-159B-3
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TYPE: PRT
CORGANISM: Homo sapiens
US-09-696-668-4
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                                                                     PLHNACSYGHYEVTELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL
                                                                                            NCHNKSAIDLAPTPQLKERLAYEPKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
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                          SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
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Sequence 4, Application US/09696668; Patent No. 6617102; GENERAL INFORMATION:

METHODS CYCLE AND ö 540 780 120 180 320 240 300 360 500 560 480 620 680 600 740 99 800 720 200 260 380 440 420 561 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADFTLKNQEGQTPLDLVS ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 201 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR SGNEEKWALLITPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 261 SGNEEKWMALLIPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL PLHNACSYGHYEVTELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 381 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKGHLSLEMVNFKHPQTHET QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 1 GFGRKDVVEYLLONGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET LGNSBADRQLLBAAKAGDVBTVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL Gaps COMPOSITIONS INVOLVED IN THE CELL ô Indels ö ; ; B Score 5582; D Pred. No. 0; 1; Mismatches APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Xu, Xianty
APPLICANT: AV, Xianty
APPLICANT: Huang, Betty
APPLICANT: OsGOVSKAYA, Valeria
TITLE OF INVENTION: TANKYRASE H, COMPOSITION
FILE REFERENCE: A-69292-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/696,668
CURRENT FILING DATE: 2002-07-23
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1 99.98; Query Match Best Local Similarity 99.9 Matches 1064; Conservative 721 g 8

ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALS SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITOFVRNLG SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITOFVRNLG MGHKELKEIGINAYGHRHKLIKGVERLISGQGLNPYLTI MGHKELKEIGINAYGHRHKLIKGVERLISGQGLNPYLTI MGHKELKEIGINAYGHRHKLIKGVERLISGQGLNPYLTI MGHKELKEIGINAYGHRHKLIKGVERLISGQGLNPYLTI SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKCKW SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKCKW NEFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS RSCYICHRQLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVT RNLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS RSCYICHRQLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVT NA XAANG HUANG, Xin Chan, Evan Xu Xaang Huang, Betty RNCENTON TANKYRASE H, COMPOSITIONS Invol SWCE: 2000-40-25 ICATION NUMBER: US 09/696,668 NG DATE: 2000-10-25 ICATION NUMBER: US 09/427,154 NG DATE: 1999-10-25 SEQ ID NOS: 17 PRACENTIN VERSION 3.1 PATENTIN VERSION 3.1 PATENTIN VERSION 3.1 PATENTIN VERSION 3.1 PATENTIN VERSION 3.1	441 ALICAASEPPERROCCELLERGANISECTREPLES TO THE HIT
Query Match 99.9%; Score 5582; DB 2; Length 1240; Best Local Similarity 99.9%; Pred. No. 0; 0.0 Matches 1064; Conservative 1; Mismatches 0, Indels 0; Gaps 0; 0.0 QY 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPHARDNANYT 200 0.0 Db 141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPHARDNANYT 200 0.0 QY 61 PLHEAAIKGKIDVCTVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120 1.0 Db 201 PLHEAAIKGKIDVCTVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 260 2.0 QY 121 SGNEEKWAALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180 1.0 Db 261 GINERKWAALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180 2.0 Db 261 JLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTL 240 3.0 Db 262 JLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTL 380 3.0 Db 321 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTL 380 3.0 Db 321 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEWEVSLLLSYGADPTL 380 3.0 Db 331 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEWEVTRIKKHLSLEMYNFKHPQTHET 300 3.0 Db 331 ALHCAAAASPYPRRKQICELLRKGANINEKTRETTPLHVASEKAHDUVVKHEAKV 360 3.0	RESULT 7 US-09-843-159B-9 ; Sequence 9, Application US/09843159B ; PAPLICANT: Luo, Yin ; APPLICANT: Chan, Evan ; APPLICANT: Chan, Evan ; APPLICANT: Chan, Evan ; APPLICANT: Huang, Betty ; TITLE OF INVENTION: Tankyzee H, Compositions Involved in the Cell Cycle and Methods c ; TITLE OF INVENTION: 2001-04-25 ; PRIOR PLILING DATE: 2001-04-25 ; PRIOR FILING DATE: 2000-10-25 ; PRIOR PLILING DATE: 1999-10-25 ; PRIOR PLILING DATE: 1999-10-25 ; NUMBER OF SEQ ID NOS: 17 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 9 ; LENGTH: 1100

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ICKLILLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600
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                                                                                               Sequence 2, Application US/09427154
Patent No. 6589725
GENERAL INFORMATION:
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Matches 1059; Conservative
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Pred. No. 0;
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       FEATURE:
, OTHER INFORMATION: synthetic mutant US-09-843-1598-9
                                            99.94;
ORGANISM: Artificial sequence
                                            Query Match
Best Local Similarity 99.9
Matches 1064; Conservative
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APPLICANT: Luo, Wing
APPLICANT: Xu, Xiang
APPLICANT: Muang, Betty
APPLICANT: Huang, Betty
TITLE OF INVENTION: TANKYRASE H, COMPOSTIONS INVOLVED IN THE OTTILE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68292-DJB/RMS/DAV
CURRENT APPLICATION NUMBER: US/09/427,154
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 9
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                              SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
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US-09-849-602-26
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APPLICANT: Toma, Salvatore
APPLICANT: Toma, Salvatore
APPLICANT: Toma, Salvatore
TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Rela
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
FILE REPERSIVE: PHRM-0043
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 5
LENGTH: 1166
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661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
                                                                                                                                                               ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
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                                          PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
                                                                                            VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
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CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (1102)..(1102)
CTHER INFORMATION: n is any nucleic acid
NAME/KEY: misc_feature
LOCATION: (2650)..(2650)
CTHER INFORMATION: n is any nucleic acid
US-09-350-982C-5
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GENERAL INFORMATION:
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Best Local Similarity
Matches 1056; Conserv
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Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
CONTRY: USA
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82.7%; Pred. No. 0;
iive 97; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 82.7%
Matches 882; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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STRANDEDNESS: single
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COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
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US-09-196-387-2
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96.0%; Score 5363.5; DB 2; Length 1227;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1035; Conservative 3; Mismatches 25; Indels 3;
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GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REPERENCE: L0461/7105(JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
WUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: PAT
TYPE: PRT
CRGANISM: Homo sapiens
US-09-849-602-26
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909 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE
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1327 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                               COUNTRY:
                US-09-841-835-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-841-835-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                 225 GFGRKDVVEHLLQMGANVHARDDGGLIPLHNACSFGHAEVVSLLLCQGADPNARDNWNYT
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Sequence 2, Application US/09841835
Patent No. 6506587
GENERAL INPOWEMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                    ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION DATA:
PRILING DATE:
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84.9%; Score 4740.5; DB 2;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79;
                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
RELEPERNOE/POCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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84.9%; Score 4740.5; 82.7%; Pred. No. 0; ive 97; Mismatches

Best Local Similarity 82.7% Matches 882; Conservative

Query Match

ORGANISM: Homo sapiens

DB 2; Length 1327; Indels

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; OKGANISM: no:
US-09-972-115A-8
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                     QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
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                                                                       421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL
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; Sequence 8, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
; APPLICANT: Walczyslaw, Płatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US 60/128,577
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 8
; LENGTH: 1327
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                                    345 SGNEEKLMALLTPLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLLQHGADVHAKDKGGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGSNRVKIVQLLLQHGADVHAKDKGDLV
                                                                                                                                                                 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL
                                                                                                                                                                                                                                                                                                                                                                                        PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLI PLHNAASYGHVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               839 VEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKE
1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLLRHGADPNARDNWNYT
                                                                                                                                                      NCHNKSAI DLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
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Arg, Ser, Thr, Ile,
Leu, a stop codon, T
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Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at location 17 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
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                                                                                                                                                  at location 10 stands for Lys, Asn, Arg, Ser, Thr, Ile, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at location 13 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at location 14 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at location 19 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at location 23 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                    at location 12 stands for Lys, Asn, Arg, Ser, Thr, Ilv
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at location 16 stands for Lys, Asn, Arg, Ser, Thr, Il.
Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Cys, or Phe.
                                                                                                                                                                                                                                                         stands for Lys, Asn, Arg, Ser, Thr, Il Val, Gln, His, Pro, Leu, a stop codon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stands for Lys, Asn, Arg, Ser, Thr, Il
Val, Gln, His, Pro, Leu, a stop codon,
                                                  Asn,
Pro,
OTHER INFORMATION: The 'Xaa' at location 9 stands for Lys, OTHER INFORMATION: Met, Glu, App, Gly, Ala, Val, Gln, His, OTHER INFORMATION: yr, Trp, Cys, or Phe.

NAMEKKEY: misc feature
LOCATION: (10). (10)
OTHER INFORMATION:
                                                                                                                                                                                                                                                         at location 11 B
Asp, Gly, Ala, V
Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at location 18 s
Asp, Gly, Ala, V
Cys, or Phe.
                                                                                                                                           OCTHER INFORMATION: The 'Xaa' OTHER INFORMATION: Met, Glu, OTHER INFORMATION: Tyr, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glu,
Trp,
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Trp,
                                                                                                                                                                                                                                                             Xaa'
Glu,
Trp,
                                                                                                                                                                                                                                                                                                                                                LOCATION: (12, .....)
OTHER INFORMATION: The 'Xaa'
OTHER INFORMATION: Met, Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xaa'
Glu,
Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: The 'Xaa', OTHER INFORMATION: Met, Glu, OTHER INFORMATION: Tyr, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glu,
Trp,
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Glu,
Trp,
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Glu,
Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glu,
Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: The 'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: The 'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: The 'Xaa' OTHER INFORMATION: Met, Glu, OTHER INFORMATION: Tyr, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (21)...(21)
OTHER INFORMATION: The 'Xaa'
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Trp,
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OTHER INFORMATION: Met, Glu,
OTHER INFORMATION: Tyr, Trp,
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OTHER INFORMATION: The '
OTHER INFORMATION: Met,
OTHER INFORMATION: Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Met,
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ION: The '
ION: Met,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Met, OTHER INFORMATION: Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION: The INFORMATION: Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Tyr,
NAME/KEY: misc_feature
LOCATION: (14)...(14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Tyr,
NAME/KEY: misc_feature
LOCATION: (18) ...(18)
OTHER INFORMATION: The
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Met,
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                                                                                                                                                                                           OTHER INFORMATION: Tyr, NAME/KEY: misc feature LOCATION: (11)..(11)
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                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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LOCATION: (16)..(16)
OTHER INFORMATION: The
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NAME/KEY: misc_feature
LOCATION: (19)..(19)
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LOCATION: (22)..(22)
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LOCATION: (23)..(23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (20)..(20)
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Leu, a stop codon,
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Leu, a stop codon, '
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a stop codon,
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a stop codon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arg, Ser, Thr, Ile,
Leu, a stop codon,
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Leu, a stop codon,
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a stop codon,
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a stop codon,
                                                1178 NERMLFHGSPFINAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPTH 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arg,
Leu,
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Leu,
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Leu,
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Leu,
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Pro,
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Pro,
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Pro,
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Pro,
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Pro,
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                                                                                     NAME/KEY: misc feature
LOCATION: yr, Trp, Cys, or Phe.
OCHER INFORMATION: The 'Xaa' at location 7 stands for Lys,
OTHER INFORMATION: The 'Xaa' at location 7 stands for Lys,
OTHER INFORMATION: Yr, Trp, Cys, or Phe.
LOCATION: (9)...(8)
OCHER INFORMATION: yr, Trp, Cys, or Phe.
LOCATION: (9)...(8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (4)...(4)
OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His,
OTHER INFORMATION: yr, Trp, Cys, or Phe.
NAME/KEY: misc_feature
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OTHER INFORMATION: The 'Xaa' at location 8 stands for Lys, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, OTHER INFORMATION: yr, Trp, Cys, or Phe.

LOCATION: (9)..(9)
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OTHER INFORMATION: The 'Xaa' at location 5 stands for Lys,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His,
OTHER INFORMATION: yr, Trp, Cys, or Phe.
LOCATION: (6)...(6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (2)...(2)
OTHER INFORMATION: The 'Xaa' at location 2 stands for OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, OTHER INFORMATION: yr, Trp, Cys, or Phe.
                                                                                                                                                                                                                                                                                                                 APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Wieczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REPREBUCE: 080/0303C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR PILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                   Sequence 2, Application US/09972115A Patent No. 6599728
                                                                                                                                                                                                                                                                                                APPLICANT: Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JAME/KEY: misc feature
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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285 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 344 121 SGNEEKAMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180	O PLENAKSIGHIEVIELLUKRAKAKVUNAHILLUGE FILDERASKAK BEVOSLILISIGARFILLI I NCHNKSAIDLAPTPQLKERLAYERKGHSLLQAAREADVTRIKKHLSLEMVNFKHPOTHET 3	525 AİHÇAAASPYPKRKÖJCELLERKGANINEKTKEFLIPLHVASEKAHNDVVEVVVKHEAKV 584 361 NALDNIGQTSILHRAAYCGHLQTCRILLSYGCDPNIISLQGFTALQMGNBNVQQLLQEGIS 420 585 NALDNIGQTSLHRAAYCGHLQTCRILLSYGCDPNIISLQGFTALQMGNBNVQQLLQEGIS 644 421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480 615 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 101 645 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 704	1 2 1 2	PDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGH pdnvncrdtogrhstplhlagxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	മെമെ	839 VEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKE 898	•
8 8 8 8	\$ 2 5 5	8 8 8 8	6 6 6	8 6 8 6 8	8 8 8 8	8 8 8 8 8	8 & 8
NAME/KEY: misc_feature LOCATION: (24)(24) LOCATION: (24)(24) OTHER INFORMATION: Met, Glu, Amp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe. LOCATION: (25) COTHER INFORMATION: The 'Xaa' at location 25 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: The 'Xaa' at location 25 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Andrew Lyshamman.	irp, CyB, or rne. Xaa' at location 26 stands for LyB, ABn, Arg, Glu, ABp, Gly, Ala, Val, Gln, HiB, Pro, Leu, Trp, CyB, or Phe.	OTHER INFORMATION: The 'Xaa' at location 27 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe. NAME/KEY: misc_feature LOCATION: (28): (28) COTHER INFORMATION: The 'Xaa' at location 28 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: The 'Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, NAME/KEY: misc feature NAME/KEY: misc feature	LOCATION: (29) (29) (29) (29) (29) (29) (29) (29) (29) (29) (20) (2	Trp, Cys, or Phe. 'Xaa' at location 31 stands for Lys, Asn, Arg, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Trp, Cys, or Phe.	OTHER INFORMATION: The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Trp, Cys, or Phe. I OCATION: (33)(33) OTHER INFORMATION: The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Trp, Cys, or Phe.	'Xaa' Glu, Trp, Xaa' Glu, Trp,	<pre>// LOCATION: (36)(36) // OTHER INFORMATION: The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile, Query Match Best Local Similarity 86.3%; Pred. No. 0; Matches 927; Conservative 7; Mismatches 131; Indels 9; Gaps 2;</pre>

RESULT 15
US-09-972-115A-4
Sequence 4, Application US/09972115A
Patent No. 6599728
GENERAL INFORMATION:

61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120

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WHER INFORMATION: The 'Xaa' at location 114 stands for Asn, Ser, Thr, or Ile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Xaa' at location 139 stands for Ile, Val, Leu, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at location 188 stands for Asn, Asp, His, or Tyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION: (110)..(110)
OTHER INFORMATION: The 'Xaa' at location 110 stands for Thr, Ala, Pro, or Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Xaa' at location 173 stands for Ile, Val, Leu, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (205)..(205)
OTHER INFORMATION: The 'Xaa' at location 205 stands for Asn, Ser, Thr, or Ile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATENION: (42)...(42)
OTHER INFORMATION: The 'Xaa' at location 42 stands for Lys, Arg, Thr, or Met.
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at location 1 stands for Thr, Ala, Pro, or Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at location 185 stands for Thr, Ala, Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at location 98 stands for Lys, Arg, Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: The 'Xaa' at location 126 stands for Lys, or Asn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Xaa' at location 174 stands for Glu, or Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Xaa' at location 202 stands for His, or Pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Xaa' at location 204 stands for Glu, or Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (144). (144) OTHER INFORMATION: The 'Xaa' at location 144 stands for Thr. NAME/KEY: misc 153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)...(153)
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                        APPLICANT: Grego, Morin B.
APPLICANT: Grego, Morin B.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR PILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SSQ TWARE: Patentin version 3.1
SSQ TWARE: Patentin version 3.1
LENGTH: 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (98)...(98)
OTHER INFORMATION: The 'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Xaa'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Xaa'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Xaa'
Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (204)...(204) OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(1)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COCATION: (139)..(139)
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LOCATION: (166)..(166)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (174)..(174)
OTHER INFORMATION: The
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LOCATION: (183)..(183)
OTHER INFORMATION: The
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LOCATION: (185)..(185)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (188)..(188)
OTHER INFORMATION: The
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LOCATION: (202)..(202)
OTHER INFORMATION: The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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COCATION: (126)..(126)
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ION: (110)..(110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAME/KEY: misc feature COCATION: (114)...(114)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAME/KEY: misc_feature
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Ser, Thr, Ile a stop codon, ION: (791). (791)
INRORMATION: The 'Xaa' at location 791 stands for Lys, Asn, Arg, Ser, Thr, Ile INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, INFORMATION: Trp, Cys, or Phe. 'Xaa' at location 215 stands for Lys, Asn, Glu, Asp, Gln, His stop codon, or Tyr. Gly Ser, Thr, Ile a stop codon, Arg, Ser, Thr, Ile Leu, a stop codon, Ser, Thr, Il Ser, Thr, Ile, Asp, or Phe. OTHER INFORMATION: The 'Xaa' at location 227 stands for His, Arg, Pro, or Leu. NAME/KEY: misc feature LOCATION: (228)..(228) 'Xaa' at location 213 stands for Ser, Gly, Arg, or Cys. or Tyr. or Leu. or Leu. 'Xaa' at location 667 stands for Tyr, Cys, Ser, or Phe 'Xaa' at location 207 stands for Asn, Asp, His, or Tyr or Phe NAME/KEY: misc feature LCCATION: (741)..(741) OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu. NAME/KEY: misc feature LCCATION: (763)..(763) Arg, Leu, Arg, Leu, Arg, Leu, ION: (228).. (228)
INFORMATION: The 'Xaa' at location 228 stands for Asn, Asp, His, Cys, Ser, 'Xaa' at location 211 stands for Gln, Arg, Pro, at location 727 stands for His, Arg, Pro, or Asn. ION: (735)..(735) | INFORMATION: The 'Xaa' at location 735 stands for Glu, or Asp. ION: (763)..(763) INFORMATION: The 'Xaa' at location 763 stands for Leu, or Phe. or Asp Asn, Pro, Asn, Pro, Asn, Pro, Asn, Pro, INFORMATION: The 'Xaa' at location 790 stands for Lys, INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, INFORMATION: Tyr, Trp, Cys, or Phe. Lys, His, Lys, His, NAME/KEY: misc feature LOCATION: (7647..(764) JTHER INFORMATION: The 'Xaa' at location 764 stands for Tyr, Lys, His, ION: (237)..(237)
INFORMATION: The 'Xaa' at location 237 stands for Glu, INFORMATION: The 'Xaa' at location 238 stands for Asn, INFORMATION: , Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, 'Xaa' at location 725 stands for Lys, NAME/KEY: misc_feature LOCATION: (789)...(789) OTHER INFORMATION: The 'Xaa' at location 789 stands for OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, OTHER INFORMATION: Tyr, Trp, Cys, or Phe. INFORMATION: The 'Xaa' at location 787 stands for INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, INFORMATION: Tyr, Trp, Cys, or Phe. INFORMATION: The 'Xaa' at location 788 stands for INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, INFORMATION: Tyr, Trp, Cys, or Phe. 'Xaa' NAME/KEY: misc feature
.LOCATION: (213)..(213)
OTHER INFORMATION: The ')
NAME/KEY: misc feature
LOCATION: (215)..(215) LOCATION: (207)...(207)
OTHER INFORMATION: The ')
NAME/KEY: misc feature
LOCATION: (211)...(211)
OTHER INFORMATION: The ') INFORMATION: The INFORMATION: , a NAME/KEY: misc feature LOCATION: (725)..(725) OTHER INFORMATION: The CATION: (727)..(727)

THER INFORMATION: The NAME/KEY: misc feature LOCATION: (667)..(667) INFORMATION: The NAME/KEY: misc feature LOCATION: (788)..(788) YKEY: misc feature TION: (727)..(727) NAME/KEY: misc feature LOCATION: (791)..(791) NAME/KEY: misc feature LOCATION: (227)..(227) NAME/KEY: misc feature NAME/KEY: misc feature LOCATION: (238)..(238) KEY: misc feature
10N: (735)..(735) /KEY: misc feature TION: (787)..(787) NAME/KEY: misc feature OTHER INFORMATION: Tyr NAME/KEY: misc feature

	LOCATION: (792)(792) OTHER INFORMATION: The 'Xaa' at location 792 stands for Lys, Asn, Arg, Ser, Thr, Ile	DD 407 CHNKSAIDLAPTPQLKERLAYEFKGHSLLQAARBADVIRIKKHLSLEMVNFKHPQTHETA 466
	, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe. Tyred Trp, Cys, or Phe.	Qy 302 LHCAAASPYPKRQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVN 361
	OTHER INFORMATION: The 'Xaa' at location 793 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: The 'Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe. NAME/KEY: MISC_Eature	362 ALDNLGQTSLHRAAYGGHLQTCRLLLSYGCDPNIISLQGFTALQMGNBNVQQLLQEGISL
	LOCATION: (794) (794) (794) OTHER INFORMATION: The 'Xaa' at location 794 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.	Qy 422 GNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQ 481
	NAME/KEY: misc feature LOCATION: (1957(1957) OTHER INFORMATION: The 'Xaa' at location 795 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,	Qy 482 HGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEI 541
		Qy 542 CKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSP 601
	з, Val, Gin, His, Fro, Leu,	Qy 602 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV 661
	OTHER INFORMATION: The 'Xea' at location 797 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.	662 AALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADFTLKNQEGQTPLDLVSA 72
	NAME/KAI: MISC FEBILITE LOCATION: (798)(798) CTHER INFORMATION: The 'Xaa' at location 798 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: The 'Ket, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.	94 46
	NAME/KEY: misc feature LOCATION: (799)(799) OTHER INFORMATION: The 'Xaa' at location 799 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,	Qy 782 FSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEM 841
	OTHER INFORMATION: Tyr, Trp, Cys, or Phe. NAME/KRY: misc feature LOCATION: (800)(800) OTHER INFORMATION: The 'Xaa' at location 800 stands for Lys, Asn, Arg, Ser, Thr, Ile	Qy 842 GHKELKEIGINAYGHRHKLIKGVGRLISGQQGLNPYLTLNTSGSGTILLDLSPDDKEFQS 901
	Val, Gin, His, Pro, Leu, a st	Qy 902 VEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHA 958
	OTHER INFORMATION: The 'Xaa' at location 801 stands for Lys, Asn, Arg, Ser, Thr, 11e OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe. NAME/KSY: misc feature	Qy 959 NERMLFHGSPFVNALIHKGFDERHAYLGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVH 1018
5 m x		Qy 1019 KDRSCYICHRQLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSV 1065
& 8	2 FGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTP 61	Search completed: December 18, 2006, 17:37:18 Job time : 39.577 secs
දු දු	62 LHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLJGEYKKDELLESARS 121 	
상 원	122 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVP 181 	
è 9	182 LHNACSYGHYBYTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN 241 	
કે	242 CHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETA 301	

6 B 6 B 6 B 6

GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

December 18, 2006, 17:27:10 ; Search time 32.8048 Seconds (without alignments) 3123.657 Million cell updates/sec Run on:

Title: Perfect score:

US-10-616-101-3 5585 1 GFGRKDVVBYLLQNGASVQA.....AMKWAHSPPGHHSVTGRPSV 1065 Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

i		مد			SUMMARIES	
Result No.	Score	Match	Query Match Length DB	80	ID	Description
-1	877.5	15.7	1765	~	T42714	3,
~	877.5	15.7	_	7	T42716	m
ო	875.5	15.7		~	A55575	'n
4	873.5	15.6	П	7	T42713	3, spli
2	871.5	15.6		7	T42715	m
9	860.5	15.4		~	S37431 ·	7
7	844	15.1		7	B35049	٦,
ω	844	15.1	1880	~	A35049	7
σ	842	15.1		-	SJHUK	٦,
10	839.5	15.0	1848	~	S37771	ankyrin, erythrocy
11	837.5	15.0		~	149502	- 1
12	834	14.9	1549	~	T13940	ankyrin - fruit fl
13	814.5	14.6	2039	~	T15347	ankyrin-related un
14	628	11.2	791	~	T42691	hypothetical prote
15	545.5	9.8	1411	~	830355	alpha-latroinsecto
16	514	9.5	934	Н	H71274	probable ankyrin -
17	496.5	8.9	1062	7	T30255	inversin - mouse
18	491.5	8.8	1062	7	T14151	Inv protein - mous
19	464.5	8.3	1401	~	S11527	alpha-latrotoxin p
20	456.5	8.2	1188	~	T19552	hypothetical prote
21	451	8.1	1058	7	D82654	
22	431.5	7.7	426	7	AE2149	
23	426	7.6	991	~	T25412	hypothetical prote
24	405.5	7.3	1184	7	T00253	
25	388	6.9	397	7	T46445	
56	372.5	6.7	2584	~	T24158	
27	372.5	6.7	2606	N	T24157	
28	363.5	6.5	1031	~	T43458 .	hypothetical prote
53	350	6.3	557	N	T46507	

hypothetical prote death-associated p	hypothetical prote	nypornetical prote hypothetical prote	myosin heavy chain	2-5A-dependent RNA	ankyrin related pr	hypothetical prote	probable ankyrin (transcription fact	myosin-light-chain	sex-determining pr	hypothetical prote	probable membrane	related to 26s pro
AC2508 137275	T21280	T32930	A59288	B45771	T19006	T27499	D84448	A42024	A55142	A34793	T21720	S48460	T50984
7 7	~ ~	7 N	~	~	~	~	~	7	~	~	7	7	7
606	1107	1435	1322	619	1016	633	247	900	1004	959	1295	1083	237
6.2	9 1	. 9.	5.5	5.5	5.4	5.4	5.4	5.3	5.2	5.1	5.1	5.1	5.1
	10.4	- 0	90	05	.5	9.5	299	5.5	290	.5	87	85	284
348.5 345	336.	31	ĕ	m	300	5		5	``	287	•••	.,	••

ALIGNMENTS

C;Accession: T42714

R;Peters, L.L; John, K.M.; Lu, F.M.; Bicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.

A;Call Biol. 130, 313-330, 1995

A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f the repeat domain.

A;Reference number: 222237; MUID:95340633; PMID:7615634

A;Reference number: 222237; MUID:95340633; PMID:7615634 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1765 <PET>
A;Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029ABB; EMBL:L40632; NID:g710548; PID:C;Genetics: ankyrin 3, splice form 2 - mouse C;Species: Mus musculus (house mouse) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 A,Map position: 10 A,Introns: 1887/1 S.Superfamily: ankyrin: ankyrin repeat homology C,Keywords: alternative splicing

22; 62 3 GRKDVVBYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTPL Query Match 15.7%; Score 877.5; DB 2; Length 1765; Best Local Similarity 30.9%; Pred. No. 4.1e-46; Matches 277; Conservative 125; Mismatches 377; Indels 117; Gaps ઠે

68 GHVEVVSELLQREANVDAATKKGNTALHIASLAGQAEVVKVLVTNGANVNAQSQNGFTPL 127 a 63 HEAAIKGKIDVCIVILQHGABPTIRNTDGRTALDLA----DPSAKAVLTGEYK---KDE 114 ઠે

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115 LLESARSGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAK 174 셤 ઠે

247 234 175 DKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYG ઠે

248 ARNDITPLHVASKRGNANMVKLLLDRGAKIDAKTRDGLTPLHCGARSGHEQVVEMLLDRS 307 235 ADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKH 294 셤 ò 295 -----PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHN 347 ò a

308 A-PILSKTKN-----HLNCVQLLLQH 339

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ankyrin 3, long splice form - human
NyAlternate names: ankyrin G
CiSpecies: Homo sapiens (man)
CiSpecies: Orderic Secondary 2009, 2352-2359, 1955
CiSpecies: 210, 2352-2359, 1955
A; Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1955
A; Reference number: A55575
A; Reference number: A55575; MUID: 95138209; PMID: 7836469
A; Reference number: A55575
A; Reference number: A5575; MIDPARC: UPIO00013C497; GB: U13616; NID: 9608024; PIDN: A; Genetics: 1-4377
A; Residues: 1-4377
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: CiSpecies (Genetics: A; Genetics: A; Genetics: CiSpecies (Genetics: CiSpecies (Genet
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188 ALHIAARKDDTKAAALLLQNDTNADVESKSGFTPLHIAAHYGNINVATLLLNRAAAUDFT 247
                                                                                                                                                 248 ARNDITPLHVASKRGNANMVKLLLDRGAKIDAKTRDGLTPLHCGARSGHEQVVEMLLDRS 307
                                                                                                                                                                                                                                                                                                         A-PILSKTKN------GLSPLHMATGGD-----HLNCVQLLLQH 339
                                                                                                                                                                                                                                                                                                                                                                                                         -----PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHN 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 NVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDL-VKDGDTDIQDLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHE
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                                                                                                              DKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NENVQQLLQEGISLGNSEADRQ--LLEAAKAGDVETVKKLCTV-QSVNCRDIEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADPTILINCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKH
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A;Cross-references: UNIPROT:Q61307; UNIPARC;UP10000027D39; EMBL:L40632; NID:g710548; PID
A;Experimental source: strain C57BL/6J; kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, 1
J. Cell Biol. 130, 313-330, 1995
A; Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | : : | | : | | : | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKHKMNVPETMNEVLD-----ISDGE 853
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                                                                                                                                                                ----NENVOOLLQEGISLGNSEADRQ--LLEBAAKAGDVETVKKLCTV-QSVNCRDIEGR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCYK---POVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLS-GSFSELSSVVSSSGT 794
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C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                               DVVEVVVXHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 NVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDL-VKDGDTDIQDLL-
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A;Accession: T42716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
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C,Accession: T42713
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L. J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1943 <PET>
A;Cross-references: UNIPROT:Q61307; UNIPARC:UP10000028367; EMBL:L40632; NID:g710548; PID:
A;Experimental source: strain C57BL/6J; kidney
                                                                                                                                                                                                       739 SCYK---PQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTE 795
LEVAEYLLOHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHE 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 ALHIAARKDDTKAAALLLQNDTNADVESKSGFTPLHIAAHYGNINVATLLLNRAAAVDFT 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 HEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLA----DPSAKAVLTGEYK---KDE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 YMAAQENHLEVVRFLLDNGASQSLATEDGFTPLAVALQQGHDQVVSLLLENDTKGKVRLP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 LLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAK 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 DKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYG 234
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                    AAQKGRIQLCALLLAHGADPILKNQEGQIPLDL-----VSADDVSALLI-AAMPPSALP
                                                                                                                                  710 VNVAEVLVNQGAHVDAQTKMGYTPLHVGCHYGNIKIVNPLLQHSAKVNAKTKNGYTPLHQ
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                                                                                                                                                                                                                                                                                                            796 GASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQ-ITLDVLVEMGHKELKEIG 850
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Matches 274; Conservative 122; Mismatches 365;
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A,Status: preliminary, translated from GB/EMBL/DDBJ
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                                                                                                                       F;201-233/Domain: ankyrin repeat homology
F;234-266/Domain: ankyrin repeat homology
F;267-299/Domain: ankyrin repeat homology
F;300-332/Domain: ankyrin repeat homology
F;333-365/Domain: ankyrin repeat homology
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                       F;73-105/Domain: ankyrin repeat homology .
F;106-138/Domain: ankyrin repeat homology .
F;139-171/Domain: ankyrin repeat homology
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QQ	460 QSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVV 519	oy	235 ADPTILINCHNKSAIDLAPTPQLKERLAVEFKGHSLLQAAREADVTRIKKHLSLEMVNFKH 294
Dp		Op	
& 2	520 NVADLWKETPLHEAAAKGKYEICKLLLQHGADPTKONRDGNTPLDL-VKDGDTDIQDLL- 577	çy	295PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHN 347
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& ସ	578RGDAALLDAAKKGCLARVKKLSSPD-NVNCRDTQGRHSTPLHLAAGYNN 625	ζζ	348 DVVEVVVKHEAKVNALDNLGGISLHRAAYCGHLGTCRLLLSYGCDPNIISLOGFTALQMG 407
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oy	626 LEVAEYILQHGADVNAQDKGGLIFLHNAASYGHVDVAALLIKYNACVNATDKWAFTFLHE 685	Qy	408nenvogliogegislgnsbadro-lierakagdvetvkkijtv-osvncrdiegr 459
Dp	: :	Db	
cy	686 AAQKGRIQLCALLLAHGADPILKNQEGQTFLDLVSADDVSALLTAAMPPSALP 738	QY	460 QSTPLHFAAGYNRVSVVFYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVV 519
op		Dp	
% qa	739 SCYKPOVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLS-GSFSELSSVVSSSGT 794	Qy	520 NVADLWKFTPLHEAAAKGKYELCKLLLQHGADPTKKNRDGNTPLDL-VKDGDTDIQDLL- 577
oy	795 EGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFERRQITLDVLVEMGHKELKEIG 850	Qy	578RGDAALLDAAKKGCLARVKKLSSPD-NVNCRDTQGRHSTPLHLAAGYNN 625
Q		Dp	
RESULT 5 T42715 ankyrin 3, splice C; Species: Mus mus C; Accession: 11-Jan-200 C; Accession: 130, A; Title: Ank3 (epi the repeat domain. A; Reference number A; Reference number A; Reference number A; Reference number A; Reference sprelimin A; Redictus: prelimin A; Redictus: prelimin A; Redictus: prelimin A; Redictus: Baclinin C; Reywords: altern C; Superfamily: ank C; Superfamily:	e form 3 - mouse usculus (house mouse) 100 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 100 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 100 # 313-330, 1995 101 # 222237; MUID:95340633; PMID:7615634 110 # 2	OY	09 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKAAFTPLHE 685
Š	115 LLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAK 174	N; Conta	ins: ankyrin 2, snort torm

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LLNRGAAVDFTARNGITPLHVASKRGNTNMVKLLLDRGGQIDAKTRDGLTPLHCAARSGH 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 DQVVELLLERGA-PLLARTKN-------GLSPLHMAAQGDHVECVK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISL 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 YEICKLLLQHGADPTKKNRDGNTPLDLV-KDGDTDIQDLLRGDAALLDAAKKGCLARVKK 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848 EEGDDTWIGDGGEYLRPEDLKELGDDSLPSSOFLDGMNYLRYSLEGGRSDSLRSFSSDRS 907
                                                                                                                                                                                                                                HEAAIKGKIDVCIVLLQHGAEPTIRNTDGRT----ALDLADPSAKAVLTGEYKKDEL---
                                                                                                                                                                                                                                                                                                                         LLOHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 HLSLEMVNFKHP-----QTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | : | : | : | : | : | : | : | : | HINDARFMGHLNIVLLLLQNGASPDVTNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642 MQIASTLILNYGAETNIVTKQGVTPLHLASQEGHTDMVTLLLDKGANIHMSTKSGL----
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                                                                                                               3 GRKDVVBYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLLRHGADPNARDNWNYTPL
                                                                                                                                                                                                                                                                                                 -LESARSGNEEKMMALLTPLNVNCHASDGRKS------TPLHLAAGYNRVKIVQL
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                        Length 3924;
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                                                                   Indels
                   Query Match 15.4%; Score 860.5; DB 2; Best Local Similarity 29.8%; Pred. No. 1.7e-44; Matches 283; Conservative 127; Mismatches 386;
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                                                                                                                                                        A,Status: preliminary
A,Molecule Lype: mRNA
A,Residues: 1.3924 «CHA>
A,Cross-references: UNIPROT:Q01484; UNIPARC:UPI0000125B19; EMBL:226634; NID:g406287; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NyMolecule type: DNA

N,Residues: 463-474, PE', 477-495 <TSE>
N,Cross-references: UNIPARC:UP1000016A55B; GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:
N,Cross-references: UNIPARC:UP1000016A55B; GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:
N,Chan, W.; Kordeli, E.; Bennett, V.
N,Chan, W.; Kordeli, B.; MUID:94075409; PMID:8253844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Tee, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.B.; Lux, S.B.; Ward, annomica 10, 858-866, 1991
annomica 10, 858-866, 1991
Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
Reference number: A40334; MUID:92009921; PMID:1833308
                                                                                                                                                                                                                                               R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal A;Reference number: A39643; MUID:91302466; PMID:1830053
                     Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004:
Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: ankyrin; ankyrin repeat homology
Keywords: alternative splicing
$2-3924/Product: ankyrin 2, long form #status predicted <MAT>
$2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MAZ>
63-95/Domain: ankyrin repeat homology <ANO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Molecule type: mRNA;
Residues: 1-1443,3585-3924 <OTT>
;Cross-references: UNIPARC:UP10000177548; EMBL:X56958
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                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
Molecule type: mRND
Residues: 1-2077 - COII>
Gross-references: UNIPARC:UPI0000177547; GB:XS6957
                                                                                      submitted to the EMBL Data Library, September 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GDB:127607; OMIM:106410; Map position: 4425-4427
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Species: Homo sapiens (man)
                                                                                                               Reference number: S37431
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Anytin 1, erythrocyte splice form 2 - human
NiAlternate names: ankyrin 2.1, erythrocyte; ankyrin-R
NiContains: ankyrin 2.2, erythrocyte
NiContains: ankyrin 2.2, erythrocyte
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Aloue 1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004
Aloue 1990 #sequence for human erythrocyte ankyrin.
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                         TPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNI
                                                        433 SNVKVETPLHMAARAGHTEVAKYLLONKAKVNAKAKDDOTPLHCAARIGHTNMVKLLLEN
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A;Molecule type: mRNA
A;Residues: 1-1880 <LAM>
A;Cross-references: UNIPROT:P16157; UNIPARC:UPI0000177545; GB:M28880
C;Genetics:
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                                                                                                                      Rilambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
Affitle: CDNA aequence for human erythrocyte ankyrin.
A;Reference number: A35049; WUID:90175370; PMID:1689849
A;Accession: B35049
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C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splinting
F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
P;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N;Contains: ankyrin 2.2, erythrocyte
C;Species: Homo maplens (man)
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C;Accession: B35049
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F;110-143/JOMBAIN: ankyrin repeat homology cAN03>
F;143-171/Domain: ankyrin repeat homology cAN04>
F;172-204/Domain: ankyrin repeat homology cAN05>
F;205-237/Domain: ankyrin repeat homology cAN05>
F;218-270/Domain: ankyrin repeat homology cAN08>
F;213-303/Domain: ankyrin repeat homology cAN09>
F;310-402/Domain: ankyrin repeat homology cAN10>
F;370-402/Domain: ankyrin repeat homology cAN11>
F;403-435/Domain: ankyrin repeat homology cAN11>
F;403-468/Domain: ankyrin repeat homology cAN13>
F;405-501/Domain: ankyrin repeat homology cAN13>
F;405-501/Domain: ankyrin repeat homology cAN14>
F;605-501/Domain: ankyrin repeat homology cAN14>
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A;Cross-references: GDB:118737; OMIM:182900
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Modecule type: mRNA
A;Residues: 1-1856 (LLMA)
A;Cross-references: UNIPARC:UPI0000177546
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R;Davis, L.H.; Bennett, V.
N. Biol. Chem. 265, 10589-10596, 1990
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A;Reference number: A35443; MUID:90285190; PMID:2141335
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A;Residues: 910-929 <HER>
A;Cross-references: UNIPARC:UP10000173DD0
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1022 SRYGESYLDQILN 1034
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          A,Map position: 8pl1.2-8pl1.2
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing, cytoskeleted.
E;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAI>
F;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F;4-76/Domain: ankyrin repeat homology <AN01>
F;77-109/Domain: ankyrin repeat homology <AN02>
F;110-142/Domain: ankyrin repeat homology <AN03>
F;110-142/Domain: ankyrin repeat homology <AN04>
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llarity 25.7%; Pred. No. 5.6e-44;
Conservative 151; Mismatches 355; Indels 306;
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A;Cross-references: GDB:118737; OMIM:182900
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F;601-633/Domain: ankyrin
F;634-666/Domain: ankyrin
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Kyesiduses 1-18B «LUI»
A;Crose-references: UNIPROT:P16157; UNIPARC:UPI0000167B64; EMBL:X16609; NID:928701; PIDN:
A;Accession: A33219
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A;Residues: 2-7,'X',9-17,'X',19-20,'T',22-30;733-749,'A',751-753;828-833,'X',835-855,'X',
X',1367;1383-1427;1601-1630;1686-1698,'D',1700;1763-1772 <LUX>
A;CTS67;1383-1427;1601-1630;1686-1698,'D',1700;1763-1772 <LUX>
A;CTS8-references: UNIPARC:UP10000173DC3; UNIPARC:UP10000173DC4; UNIPARC:UP10000173DC5;
DCA; UNIPARC:UP10000173DCB; UNIPARC:UP10000173DCC; UNIPARC:UP10000173DCD; UNIPARC:UP10000
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Jochem. Blopbys. Res. Commun. 204, 453-460, 1994
Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
Reference number: PC2220; MUID:95071348; PMID:7526850
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C;Species: 30-Sep-1911 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-191 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: $08275; A33219; PC2220; A35443
R;Lux, S.E.; John, K.M.; Bennett, V.
Nature 344, 36-42, 1990
A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated A;Reference number: $08275; MUID: 90158830; PMID: 2137557
                                                                                                                                                                                                                                                                                                                                               ----YKPQVLNGVRSPGATADALSSGPSSPSSLS----AASSLDN
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                                   Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
Contains: ankyrin 2.2
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anxylin, error butter, the mouse)
C;Dete: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
A;Determeder, C:s; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J, Biol. Chem. 268, 9533-9540, 1993
A;Reference number: 837771; MUD:93252825; PMID:8486643
A;Recession: 837771
A;Retauts: prediminary
A;Recession: 837771
A;Residues: l-1848 calr.
A;Residues: l-1848 calr.
A;Residues: l-1848 calr.
C;Superfamily: ankyrin repeat homology canols
C;Reywords: alternative splicing
C;Reywords: alternati
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1022 SRYGESYLDQILN 1034
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                                                                     Residues: 'X',5,'X',7-12;403-417,'X',419-422,'H',424,'LQ';797-800,'L',802-814;862-863,
;Cross-references: UNIPARC:UP10000173DD1; UNIPARC:UP10000173DD2; UNIPARC:UP10000173DD3
                                                                                        Cidenetics:
Cidenetics:
Aircross reference.
Cidenetics:
Aircross references: GDB:118737; OMIM:182900
Aircross-references: GDB:118737; OMIM:182900
Cisuperfamily: ankyrin, i erythrocyte form 1 #seatus predicted <MAI2>
F;2-827/Domain: ankyrin repeat homology <AN01>
F;2-827/Region: anion exchange protein blinding
F;44-76/Domain: ankyrin repeat homology <AN02>
F;110-142/Domain: ankyrin repeat homology <AN05>
F;143-171/Domain: ankyrin repeat homology <AN05>
F;228-277/Domain: ankyrin repeat homology <AN06>
F;238-277/Domain: ankyrin repeat homology <AN09>
F;238-270/Domain: ankyrin repeat homology <AN09>
F:238-270/Domain: ankyrin repeat homology <AN09>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 NRVKIVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 GNVIMVRLLLDRGAQIETKTKDELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPI 309
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llarity 25.5%; Pred. No. 7.5e-44;
Conservative 152; Mismatches 356; Indels 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1766-798/Domain: ankyrin repeat homology <AN23.
1828-1382/Domain: 62K #status predicted <DOM2>.828-1382/Region: spectrin binding
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F;601-63/Jomain: ankyrin repeat homology
F;64-666/Domain: ankyrin repeat homology
F;667-699/Domain: ankyrin repeat homology
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F;304-336/Domain: ankyrin repeat ho
F;337-369/Domain: ankyrin repeat ho
F;303-402/Domain: ankyrin repeat ho
F;403-435/Domain: ankyrin repeat ho
F;403-468/Domain: ankyrin repeat ho
F;469-501/Domain: ankyrin repeat ho
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535-567/Domain: ankyrin repeat
568-600/Domain: ankyrin repeat
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                                  A; Molecule type: protein
A; Residues: 'X',5,'X',7-1
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Best Local Similarity
Matches 279; Conserv
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;Molecule type: mRNA;
;Residues: 1-1862 <RES>
;Cross-references: UNIFROT:Q02357; UNIPARC:UPI000002921E; GB:M84756; NID:g191939; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281.285, 1992
A.Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory dom≀
A,Reference number: 149502; MUID:92345717; PMID:1386265
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                                                                                                                                                                                                                                                                                                                                            Species: Mus musculus (house mouse)
Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | || : :: ||| ||:
306 HMAAQGDHLDCVRLLLQYNAE------ID-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A journal to analyzin; ankyzin repeat homology C; Keywords: alternative splicing F; 40-72/Domain: ankyzin repeat homology <AN01>F; 40-72/Domain: ankyzin repeat homology <AN02>F; 106-138/Domain: ankyzin repeat homology <AN03>F; 106-138/Domain: ankyzin repeat homology <AN03>F; 106-20/Domain: ankyzin repeat homology <AN05>F; 201-233/Domain: ankyzin repeat homology <AN05>F; 201-233/Domain: ankyzin repeat homology <AN06>F; 201-233/Domain: ankyzin repeat homology <AN06>F; 201-233/Domain: ankyzin repeat homology <AN09>F; 201-235/Domain: ankyzin repeat homology <AN10>F; 201-235/Domain: ankyzin repeat homology <AN10>F; 306-380/Domain: ankyzin repeat homology <AN11>F; 498-530/Domain: ankyzin repeat homology <AN11>F; 498-530/Domain: ankyzin repeat homology <AN11>F; 498-530/Domain: ankyzin repeat homology <AN11>F; 561-596/Domain: ankyzin repeat homology <AN11>F; 561-596/Domain: ankyzin repeat homology <AN11>F; 561-596/Domain: ankyzin repeat homology <AN18>F; 561-596/Domain: ankyzin repeat homology <AN18>F; 561-596/Domain: ankyzin repeat homology <AN18>F; 561-652/Domain: ankyzin repeat homology <AN18>F; 561-652
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Db 288 SRTKDLL	Qy 458 GRQSTPLHFAAGYNRVSVVBYLLQHGADVHAXDKGGLVPLHNACSYGHYBVAELLVXHGAA	0	RESULT 14 142691 hypothetical protein DKFZp434D2328.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T42691 R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann submitted to the Protein Sequence Database, November 1999 A;Reference number: Z22230
(91208871) (8',1950, (208875; 1934-193	A,Cross-references: UNIPARC:UPI000007878C; EMBL:U50071; NID:g1208871; PID:g1208874; PIDN A,Accession: T1345 A,Accession: T1345 A,Accession: T1345 A,Recule type: DNA A,Residues: 1-1718, YWEELNRL',1727,'D','ES',1942,'PSPAQRS',1950,'IVAES',1956-1957,'EQVPH A,Residues: 1-1718, YWEELNRL',1727,'D','ES',1942,'PSPAQRS',1950,'IVAES',1956-1957,'EQVPH A,RESIDEBERHSQHEDHEGST' <ga4-yord c<="" contractors="" td=""><td>A; Residues: 831-852, GGG', 856-1319, IG', 1322-1595, DA', 1598-1718, KWEELNRL', 1727, 1799, RV 1945-1947, VT', 1950, '8H', 1975, 'SBSP', 1980-1981, SPTRRSVEPEEHRHS', 1984-1985, 'EDHEGS', IA; Cross-references: UNIPARC:UPI000017754A; GB:U21731 A; Accession: C57282 A; Accession: C5728 A; Accession: C57282 A; Accession: C5728</td><td>Qy 123 NEEKAMALLTPIAVNCHASDGRKSTP-LHLAAGYNRVKIVQLLIQHGADVHAKDKGDLVP 181 :</td></ga4-yord>	A; Residues: 831-852, GGG', 856-1319, IG', 1322-1595, DA', 1598-1718, KWEELNRL', 1727, 1799, RV 1945-1947, VT', 1950, '8H', 1975, 'SBSP', 1980-1981, SPTRRSVEPEEHRHS', 1984-1985, 'EDHEGS', IA; Cross-references: UNIPARC:UPI000017754A; GB:U21731 A; Accession: C57282 A; Accession: C5728 A; Accession: C57282 A; Accession: C5728	Qy 123 NEEKAMALLTPIAVNCHASDGRKSTP-LHLAAGYNRVKIVQLLIQHGADVHAKDKGDLVP 181 :

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28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 YNGHHQALEVLLQSLVDLDIRDEKGRTALDLAAFKGHTECVEALIN------QGAS 440
                                                                                                                                                                                                                                                                                                                              | | | : | : : | : : | HIT | : | | : : | : : | HITAAASTHGALCLELLVNNGADVNIQSKDGKSPLHM-----TAVHGRFTRSQTLIQNGG 127
                                                                                                                                                                                                                                                                                                                                                                                                        ----STP----LHLAAGYNRVKIVQLLLQHGADVH 172
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                                                                                                                                                                                                       Gaps
A,Accession: T42691
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-791 <AAA>
A,Cross-references: UNIPROT: 09UFA4; UNIPARC: UP100006DC92; EMBL:AL133087
A,Experimental source: adult testis; clone DKPZp434D2328
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                                                                                                                                                              11.2%; Score 628; DB 2; Length 791;
llarity 27.7%; Pred. No. 4.3e-31;
Conservative 119; Mismatches 313; Indels 174;
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                                                                                                                                                              Query Match
Best Local Similarity
Matches 232; Conserv
                                                                                                          C;Genetics:
A;Note: DKFZp434D2328.1
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C;Species: Latrodectus mactans tredecimguttatus (black widow spider)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Accession: $3055-$22864
Eur. J. Blochem. 213, 121-127, 1993
A;Title: Cloning and structural analysis of alpha-latroinsectotoxin cDNA. Abundance of an A;Reference number: $30355; MUID:93238678; PMID:8477689
A;Accession: $30355
A;Molecule type: mRNA
A;Residues: 1-1411 KKIY.
A;Coss-references: UMIPROT:002989; UMIPARC:UPI000007A3C2; EMBL:Z14086; NID:99536; PIDN:CA;Coss-references: UMIPROT:002999; UMIPARC:UPI000007A3C2; EMBL:Z14086; NID:99536; PIDN:CA;Coss-references: UMIPROT:00299; UMIPARC:UPI000007A3C2; EMBL:Z14086; NID:99536; PIDN:CA;Coss-references: UMIPROT:002999; UMIPARC:UPI000007A3C2; EMBL:Z14086; NID:99536; PIDN:CA;Coss-references: UMIPROT:002999; UMIPARC:UPI000007A3C2; EMBL:Z14086; NID:99536; PIDN:CA;Coss-references: UMIPROT:002999; UMIPARC:UPI00007A3C2; EMBL:Z14086; UMIPARC:UPI001099; AMIZ-PI001-1032/Domain: ankyrin repeat homology AMIZ-PI001-1032/Domain: AMIZ-PI001-103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 ATLONNLSVSKLLAGKGAYLNDGDANGMTPLHYAAMTGNLEMVDFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.8%; Score 545.5; DB 2; Best Local Similarity 23.7%; Pred. No. 1.5e-25; Matches 239; Conservative 136; Mismatches 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLR---
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alpha-latroinsectotoxin precursor - black widow spider (fragment)

RESULT 15

 1312 ENLLSGLIG	1312	qq
 865 ERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHR 914	865	à
 1266GALLLLDFMIRVFASKKTNFAPYGSRIKTRSAAEAQAEALIMTERF 1311	1266	QΩ
 818 NIGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGV 864	818	ò
1221 GISMSARTNDKLTQQISSKGTRSDSNSTEGKMHSENVHVRSIDVN 1265	1221	q
 758 ALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVR 817	758	ò
1166 LVRQGADVNAKGIDDLRPID-IAGEKAKAYLQSSRFLRSGHSFQ-SNEIDSFGNTH 1220	1166	q
698 LLAHGADPTLKNOEGOTPLDLVSADDVSALLTAAMPPSALPSCYKPOVLNGVRSPGATAD 757	869	è

Search completed: December 18, 2006, 17:36:01 Job time : 39.8048 secs

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us-10-616-101-3.rup

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

December 18, 2006, 17:21:50 ; Search time 213 Seconds (without alignments) 4625.078 Million cell updates/sec

US-10-616-101-3 5585 1 GFGRKDVVEYLLQNGASVQA.....AMKMAHSPPGHHSVTGRPSV 1065 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 segs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q9h2k2 homo sapien	Q800e0 gallus gall			Q4g0f2 homo sapien	-			Q59fx0 homo sapien						m ac	шnв	Q6p537 mus musculu	Q4fzm0 xenopus lae	Q574d8 rattus norv	Q574d7 rattus norv	Q4u258 mus musculu	Q4u256 mus musculu	Q7z3g4 homo sapien	mus m	Q12955 homo sapien	O5czh9 homo sapien	mus m	Q4u257 mus musculu	Q9n180 bos taurus	•	070511 rattus norv
	ID	TNKS2 HUMAN	Q800EO CHICK	Q6PFX9_MOUSE	TNKS1 HUMAN		Q800D9 CHICK	QSXGKS XENLA	Q4RG97_TETNG	Q59FX0_HUMAN	Q8BX62_MOUSE	Q7PYH8_ANOGA	Q9VBP3_DROME	Q9XZ37_DROME	Q4S372 TETNG	Q3UES3 MOUSE	Q8BXH7 MOUSE	Q6P537 MOUSE	Q4FZM0 XENLA	Q574D8_RAT	Q574D7_RAT	Q4U258_MOUSE	Q4U256 MOUSE	Q7Z3G4_HUMAN	Q8VC68_MOUSE	ANK3 HUMAN	QSCZH9 HUMAN	Q4U259 MOUSE	Q4U257 MOUSE	O9N180_BOVIN		O70511_RAT
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de	Query Match	99.9	95.8	84.9	84.9	84.7	84.7	83.7	82.9	81.2	74.1	68.9	66.4	66.4	56.9	50.7	48.9	33.7	32.1	15.9	15.9	15.7	15.7	15.7	15.7	15.7	15.6	15.6	15.6	15.5	15.5	15.5
	Score	5582	5350	4742.5	4740.5	4732.5	4730.5	4674.5	4631.5	4532.5	4136.5	3849	3706.5	3706.5	3179	2833	2731	1883	1795.5	886	988	877.5	877.5	876.5	875.5	875.5	873.5	873.5	871.5	867.5	865	864.5
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Q7z315 homo sapien O88521 rattus norv Q01484 homo sapien Q8c8r3 mus musculu Q4rnf0 tetraodon n Q13768 homo sapien P16157 homo sapien P97582 rattus norv Q99407 homo sapien Q59fp2 homo sapien Q61302 mus musculu Q3uh42 mus musculu Q3uhp2 mus musculu Q3uhp2 mus musculu Q3uhp2 mus musculu
072315 HUMAN 088521_RAT MACZ HUMAN 08C8R3 HUMAN 08C8R3 HUMAN 013768 HUMAN P97582 RAT 099407—HUMAN 061302—MOUSE 03UHA2 MOUSE 03UHP2 MOUSE
4000000000000000000000000000000000000
1863 1762 3924 1219 4408 1719 1810 1856 1856 1899 1848 1978
8.00 1.00
863.5 863.5 860.5 854.5 811.5 842.8 842.8 840.5 840.5 839.5 839.5
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ALIGNMENTS

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REPENDINGS.

KENDINGS.1661618. PubMedaing02774, DOI:10.1042/0264-6021;5610451;

KENDINGS.2661618. PubMedaing02774, DOI:10.1042/0264-6021;5610451;

KENDINGS.2661618. PubMedaing02774, DOI:10.1042/0264-6021;5610451;

KENDINGS.2661618. PubMedaing02774, DOI:10.1042/0264-6021;3610451;

KENDINGS.2661618. PubMedaing02774, DOI:10.1042/0264-6021;3610451;

KENDINGS.2661618. PubMedaing02774, DOI:10.1042/0264-6021;3610451;

KINDINGS.2661618. PubMedaing0276. PubMedite018.

KINDINGS.26618. PubMedaing02774, DOI:10.1042/0264-6021;3610451;

KINDINGS.26618. PubMedaing02774, DOI:10.1042/0264-6021;3610451;

KINDINGS.26618. PubMedaing02774, DOI:10.104618. PubMedaing0274;

KINDINGS.26618. PubMedaing0274, DOI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048/DAI:10.1048
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License æ Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human -i-TISSUE SPECIFICITY: Highly expressed in placenta, skeletal muscle, liver, brain, kidney, heart, thymus, spinal cord, lung, peripheral blood leukocytes, pancreas, lymph nodes, spleen, prostate, testis, ovary, small intestine, colon, mammary gland, breast and breast carcinoma, and in common-type meningioma. Highly expressed in fetal liver, heart and brain.
-i-FPM: ADP-ribosylated (-auto).
-i-SIMILARITY: Contains 15 PARK respeats.
-i-SIMILARITY: Contains 1 SAM (sterile alpha motif) domain. MOI. Cell. Biol. 22:322-342 (2002).

-I- FUNCTION: May regulate vesicle trafficking and modulate the subcellular distribution of SIC2A4/GLUT4-vesicles. Has PARP activity and can modify TRFI, and thereby contribute to the regulation of telomere length.

-I- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-ribosyl) (n)-acceptor = nicotinamide + (ADP-D-ribosyl) (n+1)-acceptor.

-I- SUBUNIT: Oligomerizes and associates with TNKS. Interacts with the cytoplasmic domain of LAMPEP/Otase in SLC2A4/GLUT4-vesicles. Binds to the N-terminus of Grbl4 and TRF1 with its ankyrin repeat MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002; Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.; "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2 SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. Also found around the pericentriolar matrix of mitotic centromeres. During interphase, small fraction of TNKS2 is found in the nucleus, associated with Glycosyltransferase, Golgi stack; NAD; Nuclear protein; Repeat; PROSITE; PS50297; ANK REP_REGION; 1.
PROSITE; PS50088; ANK REPEAT; 15.
PROSITE; PS51059; PARP_CATALYTIC; 1.
PROSITE; PS50105; SAM DOMAIN; 1.
ADP-ribosylation; ANK repeat; Chromosomal protein; Tankyrase 2. /FTId=PRO_0000211334. ANK 1. ANK 2. EMBL; AF305081; AAG25674.1; ALT INIT; mRNA. EMBL; AF264912; AAG44694.1; -; mRNA. AF309033; AAK82330.1; -; mRNA. AF438201; AAL40795.1; -; mRNA. AL359707; CAC78760.1; -; Genomic DNA. AK023746; BAB14665.1; ALT_INIT; mRNA. Ensembl; ENSG0000107854; Homo sapiens. MIM; 607128; gene.
InterPro; IPR001290; PARP.
InterPro; IPR012317; PARP_catalytic.
InterPro; IPR011510; SAM.
InterPro; IPR011510; SAM.
Pfam; PF00023; Ank; 17.
Pfam; PF0044; PARP; 1.
SMART; SM00454; SAM, 1. AF329696; AAK13463.1; -; mRNA. AF342982; AAK25811.1; -; mRNA. FUNCTION, AND ADP-RIBOSYLATION. Nat. Genet. 36:40-45(2004). HGNC:15677; TNKS2. elomere, Transferase. at human telomeres."; P16157; 1N11 57 REPEAT REPEAT EMBL; EMBL; HGNC; EMBL; EMBL; HSSP;

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1027 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1086
                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 GFGRKDVVEYLLQSGANVHARDDGGLIPLHNACSFGHAEVVNLLLRHGANPNARDNWNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLHNACSYGHYEVTELLLYKHGACVNAMDLWQPTPLHEAASKNRVEVCSLLLSYGADPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLHEAAIKGKIDVCIVLLOHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                      MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450; De Rycker M., Venkatesan R.N., Wei C., Price C.M.; "Vertebrate tankyrase domain structure and sterile alpha motif (SAM) mediated multimerization." Biochem. J. 372:87-96(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY142107; AAA41650.1; -; mRNA.

R SSP; 000420; 1AWC.

R Ensembl; ENSGALG00000011438; Gallus gallus.

R GO; GO:0005634; C:inucleus; IEA.

GO; GO:0005634; C:inucleus; IEA.

GO; GO:00066471; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR001290; PARP.

R InterPro; IPR012317; PARP_catalytic.

R InterPro; IPR01550; SAM.

R InterPro; IPR01550; SAM.

R Ffam; PF00644; PARP; 1.

R Pfam; PF00644; PARP; 1.

R PARMY; SW00248; SAM, 1.

R SWART; SW00466; SAM, 1.

R SWART; SW00466; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126932 MW; 7842BF482B9229E9 CRC64;
                            Query Match 95.8%; Score 5350; DB 2; Best Local Similarity 95.0%; Pred. No. 8.5e-308; Matches 1012; Conservative 29; Mismatches 24;
                                                                                                                                                                  01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 14.
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                                                                                                                                       PRT; 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0297; ANK REP REGION; 1. PROSITE; PSS0088; ANK REPEAT; 15. PROSITE; PSS1059; PARP CATALYTIC; 1. PROSITE; PS50105; SAM DOMAIN; 1.
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                              Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANK repeat; Repeat.
SEOUENCE 1167 AA;
                                                                                                                                                                                                                                                                                                           [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                             Gallus.
NCBI_TaxID=9031;
                                                                                                                                       Q800E0 CHICK
Q800E0;
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                                                                                                                                                                     PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
                                                                                                                                                                                                                                                                                            PLHNACSYGHYEVTELL VKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NALDNIGQTSLHRAAYCCHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
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                                              Score 5582;
Pred. No. 0;
ANK 3.
ANK 4.
                                            99.94;
                                              Query Match
Best Local Similarity 99.9
Matches 1064; Conservative
 123
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NUCLECTIDE SEQUENCE.

RY STRAIN=C57BL/6, TISSUE=Brain;

RY Altschul S.F., Zeeberg B., Buctow, K.H., Schaefer C.F., Bhat N.K.,

RY DIATCHENCO.L., MARTHAIN R., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Porner A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Frange C.,

Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,

RADA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RADA S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RACHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RALES S., Loquellano A., Young A.C., Shevchenko Y., Bouffard G.G.,

RHITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RHITING M., Nadan J.W., Green E.D., Dickson M.C.,

RHITING M., Krzywinski M.I., Skalbka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalbka U., Smailus D.E.,

RH. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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REAL; BCOS07370; AAH57370.1; -; MRNA.

RISSP; Q00420; LAWC.

R Ensembl; ENSWUSG00000031529; Mus musculus.

R MG1; MG11341087; Trks.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005950; F:Nub-ADP-ribosyltransferase activity; IEA.

GO; GO:0005950; F:Nub-ADP-ribosyltransferase activity; IEA.

GO; GO:0005950; F:Nub-ADP-ribosyltransferase activity; IEA.

R GO; GO:0005950; F:Nub-ADP-ribosyltransferase activity; IEA.

R GO; GO:0005950; F:Nub-ADP-ribosyltransferase activity; IEA.

R InterPro; IPR00110; PARP.

R InterPro; IPR00110; PARP.

R InterPro; IPR001231; PARP.

R InterPro; IPR001510; SAM.

R Pfam; PF00644; SAM.

R Pfam; PF00644; SAM.

R Pfam; PR07647; SAM. 2.

R Pfam; PR076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00454; SAM; 1.
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095271; 095272;
27-MAR-2002, integrated into UniProtKB/Swiss-Prot.
01-MAY-1999, sequence version 1.
7ankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) interacting ankyrin-related ADP-ribose polymerase).
Name=TNKS; Synonyms-PARPSA, PARPL, TINI, TINFI, TNKSI;
Homo sapiens (Human).
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INTITIONAL A COMPLEX WITH POTL; TERFI AND TINF2.

IDENTIFICATION IN A COMPLEX WITH POTL; TERFI AND TINF2.

MEDLINE=22711258; PubMed=12768206; DOI=10.1038/nature01688;

Loayza D., De Lange T.;

"POTL as a terminal transducer of TRFI telomere length control.";

"POTL as a terminal transducer of TRFI telomere length control.";

"TOTALYTION: May regulate vesicle trafficking and modulate the subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP activity and can modify TERFI, and thereby contribute to the regulation of telomere length.

"TOTALYTIC ACTIVITY: NAD(+) + (ADP-D-ribosyl) (n) -acceptor = nicotinamide + (ADP-D-ribosyl) (n+1) -acceptor = nicotinamide + (ADP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
MEDLINE=2162874; PubMed=1173745; DOI=10.1128/MED.22.1.332-342.2002;
GOOK B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
                                                                                                                                                                                                    MEDLINE=99040105; PubMed=9822378; DOI=10.1126/science.282.5393.1484;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ution of the telomeric PARP, tankyrase, centrosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND PHOSPHORYLATION.
MEDLINE=20556282; PubMed=10988299; DOI=10.1074/jbc.M007635200;
MEDLINE=20556282; PubMed=10988299; DOI=10.1074/jbc.M007635200;

"Thi N.-Wa., Lodish H.P.;
"Thi N.-Wa., Lodish H.P.;
"Thankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
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-1 TISSUB SPECIFICITY: Ubiquitous; highest levels in testis.
-1 FINH: Phosphorylated on serine residues by MAPK kinases upon insulin stimulation.
-1 FTM: ADP-ribosylated (-auto).
-1 SIMILARITY: Contains 15 ANK repeats.
-1 SIMILARITY: Contains 1 SAPR catalytic domain.
-1 SIMILARITY: Contains 1 SAPR (sterile alpha motif) domain.
                                                                                                                                                                                                                         Smith S., Giriat I., Schmitt A., de Lange T.;
"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487(1998).
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                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2)
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                                                                                                                                                                                                                                                                                                                                                                                                      Smith S., de Lange T., "Cell cycle dependent localization of to nuclear pore complexes and centrosc
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EMBL; AF082557; AAC79842.1; -; mRNA.
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Mol. Cell. Biol. 22:332-342(2002).
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MEDLINE-99454782; PubMed=10523501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell Sci. 112:3649-3656(1999)
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SGNEEKLMALLTPLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLLQHGADVHAKDKGGLV 404
                                               PLHNACSYGHYEVTELLLKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSHGADFTLV
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                                                                                            NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
                                                                                                                                                           ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV
                                                                                                                                                                                                                        NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
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Name-TNKS;
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Poly-Ser.
Poly-Ser.
EST -> GHS (in isoform 2).
/Frid=VSP 004538.
/Frid=VSP 004539.
/Frid=VSP 004539.
H-A: Loss of activity; when associated
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82.7%; Pred. No. 1.3e-271;
iive 97; Mismatches 79;
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EMBL, AF082558; AAC79843.1; -; mRNA.
EMBL; AF082559; AAC79844.1; -; mRNA.
HSSP; P16157; 1N11.
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Matches 882; Conservative
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                                                                                       241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
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Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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RA STRAUSBERG R.L., Feringold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schamen C.M., Schuler G.D.,

RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Boaks S.A., McWann P.J., McKernan R.D., Mullahy S.J.,

Rownstein M.J., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human and man man and m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Chordata, Craniata, Vertebrata, Buteleostomi,
Buarchontoglires, Primates; Catarrhini, Hominidae,
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82.6%; Pred. No. 4e-271;
ive 97; Mismatches 80; Indels 9;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1327 AA; 141980 MW; 21A8309DF979CA21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO; GO:0003590; F:NDD+ ADP-ribosyltrans
GO; GO:0006471; P:Protein amino acid AD
InterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
InterPro; IPR002317; PARP_catalytic.
InterPro; IPR001660; SAM.
Pfam; PF00644; PARP; 1.
Pfam; PF00644; PARP; 1.
PRINTS; PR01415; ANKYIN.
SWART; SW00248; ANK, 15.
SWART; SW00454; SAM; 15.
PROSITE; PS500089; ANK REP REGION; 1.
PROSITE; PS500089; ANK REP REGION; 1.
PROSITE; PS50105; SAM_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE 1327 AA
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661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
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                                                                                                                                                                                                PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
                                                                                                                                                                                                                                                                                                                                             781 SPSELSSVVSSSGTEGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    839 VEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOSVEEEMOSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Spleen;
MEDILNE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLHNACSYGHYEVTELLLKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLV
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MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;
De Rycker M., Venkatesan R.N., Wei C., Price C.M.;
"Vertebrate tankyrase domain structure and sterile alpha motif (SAM)-mediated multimerization.";
Biochem. J. 372:87-96(2003).
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                                                                                                                                                                                                                                                                                                                                                              HSSP; Pi6157; 1N11.
Ensembl; ENSALG0000011438; Gallus gallus.
G0; G0:000563; C:nucleus; IEA.
G0; G0:000563; C:nucleus; IEA.
G0; G0:0006471; P:protein amino acid ADP-ribosylation; IEA.
InterPro; IPR002110; ANK.
InterPro; IPR012317; PARP_catalytic.
InterPro; IPR012317; PARP_catalytic.
InterPro; IPR012317; PARP_catalytic.
InterPro; IPR01510; SAM_c.
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SEQUENCE 1266 AA; 136212 MW; 14B8617EF930E6E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00023; Ank; 19.
Pfam; PF00644; PARP; 1.
Pfam; PF00644; SAM 2; 1.
PRNTS; PR01415; ANKYRIN.
SWART; SW00454; SAM; 15.
SWART; SW00454; SAM; 11.
PROSITE; PS50089; ANK REP REGION; 1.
PROSITE; PS50089; ANK REPRAT; 15.
PROSITE; PS51059; PARP CATALYTIC; 1.
PROSITE; PS51059; PARP CATALYTIC; 1.
                                                                                                                                                                                                                                                                                                                                             EMBL; AY142108; AAN41651.1; -; mRNA.
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                NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420
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                                                             561 NTLDTLGGTALHRAALGGHLQTCRLLLSFGSDASIVSLQGFTAAQMGNEAVQQILNESTP
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                                                                                                                                                                           421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL
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19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 5.
Chromosome 12 SCAFF15104, whole genome shotgun sequence. (Fragment). ORFNames=GSTENGO034904001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Percadontidae; Tetraodontiformes; Tetraodontidae; Tetraodontiformes; NCBL_TaxID=99883;
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Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan R.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M. Madan A., Young A.C., Shevchenko Y., Bolffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.R., Schein J.B., Schlek J.S., Schein J.B., Schlek J.S., Schein J.B., Schein J.B., Marra M.A., Schein J.B., Schein J.B., Marra M.A., Schein J.B., Marra M.A., Schein J.B., Marra M.A., Marra M.A., Schein J.B., Marra M.A., Marra M.A., Schein J.B., Marra M.A., Marra M.A., Marra M.A.
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R GO; GO:0005534; C:nucleus; IEA.

R GO; GO:0003501; F:NND+ ADP-ribosyltransferase activity; IEA.

R GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR001210; ANR.

R InterPro; IPR001230; PARP.

R InterPro; IPR001231; PARP.

R InterPro; IPR001331; PARP.

R InterPro; IPR001331; PARP.

R Pfam; PF00023; Ank; 18.

R Pfam; PF00647; SAM 2; 1.

R Pfam; PR0044; PARP; 15.

R SWART; SW0044; BAR; 15.

R SWART; SW00454; SAM; 15.

R PROSITE; PS50088; ANK REPEAT; 15.

R PROSITE; PS51059; PARP_CATALYTIC; 1.

R PROSITE; PS51059; PARP_CATALYTIC; 1.

R PROSITE; PS51059; PARP_CATALYTIC; 1.
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Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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81.6%; Pred. No. 1.1e-267;
ive 99; Mismatches 88;
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SEQUENCE 1303 AA;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                         DVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPD
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                                                                                                                                                                                                                             GRIQLCALLLAHGADPILKNQEGQTPLD-----------LVSADDV
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                                                                                SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVA
                                                                                                                                                              DTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVA
                                                                                                                                                                                                                                                                                                                                                                                                      SALLTAAMPPSALPSCYKPQ---VLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGS
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                                                                                                                                                                                                                                                                                                                                                                      770 GRIQLCALLLAHGADPIMKNOEGOTALDLATVNLPLFIVSTLYSRRAHGVFWLLLQADDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSELSSVVSSSGT----EGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDIFEREQITL
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26-APR-2005, sequence version 1.
07-FBB-2006, entry version 6.
Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase variant (Fragment).
Homo sapiens (Human).
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Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
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                   LLQEGISLGNSEADRQLLEAAKAGDVETV-
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Q59FXO;
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                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kallis M., Volff J.-W., Guigo R., Zody M.C., Meairov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEKTWWNTFLQTGANVHARDDGGLIPLHNACSFGHAEVVSLLLCHGADPNARDNWNYTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 HNACSYGHFEVTELLIKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLLNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HCAAASPYPKRKQICELLLRKGANINEKTKBFLTPLHVASEKAHNDVVEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 VKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 NEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNACSYGHYBVTELLIVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNC
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                                                                                                                                                                               Genoscope; Whitehead Institute Centre for Genome Research;
Submittend (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0006541; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR012317; PARP_catalytic.

R InterPro; IPR012317; PARP_catalytic.

R Pfam; PF00044; PARP; 1.

R Pfam; PF00044; PARP; 1.

R PRINT; PR00544; PARP; 1.

R PRINT; PR00546; PAM; 1.

R PRNST; SW00246; ANK; 13.

R SWART; SW00454; ANK; 13.

R PROSITE; PS50297; ANK REP REGION; 1.

R PROSITE; PS50098; ANK REP RAT; 13.

R PROSITE; PS51059; PAMP CATALYTIC; 1.

PROSITE; PS51059; PAMP CATALYTIC; 1.
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82.9%; Score 4631.5; DB 2;
Best Local Similarity 77.2%; Pred. No. 3.3e-265;
Matches 872; Conservative 103; Mismatches 78;
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NQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSS
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                                                                                                                                                                                                                                                                                                                            ADPNARDNWNYTPLHEAAIKGKIDVCIVILQHGADPNIRNTDGKSALDLADPSAKAVLTG
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                                                                                                                                                                                                                                                                                             9; Gaps
 Distributed under the Creative Commons Attribution-NoDerivs License
                                   R GO; GO: 0005644; C: nucleus; IEA.

R GO; GO: 0005654; C: nucleus; IEA.

R GO; GO: 000550; F: NAD+ ADP-ribosyltransferase activity; IEA.

R GO; GO: 000647; P: Protein amino acid ADP-ribosylation; IEA.

R InterPro; IPRO1210; ANK.

R InterPro; IPRO12317; PARP.

R InterPro; IPRO12317; PARP.

R InterPro; IPRO11510; SAM_2.

R InterPro; IPRO11510; SAM_2.

R Pfam; PF00644; PARP; 1.

R Pfam; PF00644; PARP; 1.

R Pfam; PR00644; PARP; 1.

R Pfam; PR00454; ANK, RAPPER RGION; 1.

R PROSITE; PS50088; ANK, REPEAT; 13.

R PROSITE; PS51059; PARP_CATALYTIC; 1.

R PROSITE; PS51059; PARP_CATALYTIC; 1.
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.6%; Pred. No. 2e-259;
Matches 842; Conservative 93; Mismatches 75; Indels 9;
                                                                                                                                                                                                                                                   1055 AA; 115234 MW; 9210519D299EB805 CRC64;
                  EMBL; AB209339; BAD92576.1; -; mRNA.
Ensembl; ENSG0000173273; Homo sapiens.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

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R Ensembl; ENSWUSG0000031529; Mus musculus.

R MG1; MG1:1341087; ThKs.

R GO; GO:0005647; ThKs.

R GO; GO:000556; F:NAD+ ADP-ribosyltransferase activity; IEA.

R GO; GO:000647; P:protein amino acid ADP-ribosylation; IEA.

R GO; GO:00647; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR001200; PARP.

R InterPro; IPR001210; PARP.

R InterPro; IPR001217; PARP_catalytic.

R InterPro; IPR01516; SAM_2.

R Pfam; PF00644; PARP; 1.

R Pfam; PF00644; SAM; 12.

R SWART; SM00248; ANK; 12.

R SWART; SM00454; SAM; REP REGION; 1.

R PROSITE; PS50088; ANK_REP REGION; 1. EMBL; AK048860; BAC33475.1; -; mRNA. STRAIN=C57BL/6J; TISSUE=Cerebellum; STRAIN=C57BL/6J; TISSUE=Cerebellum; NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE

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                                                atch 74.1%; Score 4136.5; DB 2; Length 976; cal Similarity 81.7%; Pred. No. 5.1e-236; 770; Conservative 87; Mismatches 71; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGNEEKMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLHEAASKGKIDVCIALLQHGADPSIRNSENKIPLDLADPCTRPVLTGEYRKDELLEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
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                       15-DEC-2003, integrated into UniProtKB/TrEMBL.
06-DEC-2005, sequence version 2.
07-FEB-2006, entry version 21.
ENSANGRO0000018360.
ORPNames-ENSANGG8000015871;
Anopheles gambiae str. PEST.
ENKARYOCA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Anophelinae; Anopheles.
Anophelinae; Anopheles.
NCBI TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
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GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
ANK repeat; Repeat.
SEQUENCE 1168 AA; 126988 MW; 0386A4161210012B CRC64;
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Best Local Similarity 66.5%; Pred. No. 7.2e-219;
Matches 730; Conservative 146; Mismatches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                      "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ
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PRELIMINARY;
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ANOGA
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1050 GMFGAGIYFAEHSSKSNOYVYGIGGGIGCPTHKDKSCYQCHRQLLLCRVALGKSFLQFSA 1109
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                                                                                                                                                                                                                                                                                                                                                                           771 ATAEDVKCLLODAM-------VASQGTVAGGTAAGAGAGTSQGGILSANGTL--L 816
                                                                                                                                                                                                                                                                                                                                                                                                             SGSFSELSSVVS-----EKKEVPG 807
MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., ib P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                           539 YEICKLILLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKL
                                                                                                                                                                                                 SSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGH
                                                                                                                                                                                                                                                                      VDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL
                                                                                                                                                                                                                                                                                                                                          VSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           868 - ISGOGGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRY
                                                     LLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGK
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BRESON KY, DOUGLAN MR., BOUNK J., BROAGELIP P., BROAGELIP P., BROAGER I., BERNOR B. BRANCHER P. BROAGERS W. BROCKDAN MR., BOUNK J., BROAGERIP P., BROAGERS Y., CHARLES K., DOWNOR B.C., DUNKOW B.
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874 LNPYLTLNTSGSG-----TILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYN 927
                                                                                                                                                                                                                                                                                                                                                                                                                            928 ILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGG 987
                                                                                                                                                              719 VSADDVSALLTAAMPPS----ALPSCYKPQVLNGVRSPGATADALSSGPSSPSS--LSAA 772
599 YDICKLILKHGADPMKKONRDGATPADLVKESDHDVAELLRGPSALLDAAKKGNLARVQRL 658
                                                                                                                                                                                                                                                                                            814 QFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQOG 873
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                 Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxtera E., Blazei R.G., Butenhoff C., Chaw M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshreii M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.,
                                                                                              559 VDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL
                                                                                                                                                                                           779 ATADDVKCLLQDAMATSLSQQAL-SASTQSLTSSSPAPDATAAAAPGTSSSSSAILSPT
                                                                                                                                                                                                                               773 SSLDNLSGSFSELSSV----VSSS-----GTEGASSLEKKEVPGVD--FSIT
                                 599 SSPDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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FlyBase; FBgn0027508; tankyrase.
GO; GO:0005534; C:nucleus; IEA.
GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999, sequence version 1.
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Hypothetical protein.
Name=tankyrase; ORFNames=CG4719;
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Q9X237;
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Q9XZ37_DRO
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                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                     R FlyBase; FBG0021508; tankyrase.

R GO; GO:0005534; C:nucleus; IEA.

R GO; GO:000356; F:NAD+ ADP-ribosyltransferase activity; IEA.

R GO; GO:000471; F:NAD+ ADP-ribosyltransferase activity; IEA.

R InterPro; IPR001210; PARP.

R InterPro; IPR012117; PARP.

R InterPro; IPR012117; PARP.

R InterPro; IPR012117; PARP.

R InterPro; IPR012117; PARP.

R InterPro; IPR01317; PARP.

R Ffam; PF00643; Ank; 17.

R Pfam; PF00644; PARP; 1.

R Pfam; PF00644; PARP; 1.

R Pfam; PR01445; Ank; 15.

R SMART; SM00454; ANK; 15.

R RPGSITE; PS50299; ANK REPERT; 14.

R PROSITE; PS51059; PARP CATALYTIC; 1.

R PROSITE; PS51059; PARP CATALYTIC; 1.

R PROSITE; PS51059; PARP CATALYTIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 66.4%; Score 3706.5; DB 2; Length Local Similarity 65.4%; Pred. No. 2e-210; es 717; Conservative 151; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANK repeat; Repeat. SEQUENCE 1181 AA; 127945 MW; EB6F0F94E6A3D504 CRC64;
                                Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                               EMBL; AE003752; AAF56487.1; -; Genomic_DNA
HSSP; P20749; 1K1B.
   NUCLEOTIDE SEQUENCE
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EMBL; CAAE01014752; CAG04910.1; -; Genomic_DNA.
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               SSLDNLSGSFSELSSV----VSSS
                                                                                                                                                                                                                                           KMAHSPPGHHSVTGRPS 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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048372;
19-JUL-2005, i
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                                                                                                                                                                                                                                                   PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
                                                                                                                                                                                                                                                                                                                                       659 VTPESINCRDAQCRNSTPLHLAAGYNNFECAEYLLENGADVNAQDKGGLIPLHNASSYGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         779 ATADDVKCLLQDAMATSLSQQAL-SASTQSLTSSSPAPDATAAAAPGTSSSSSAILSPT
                                                                                                                                                                                                                                                                                                                           SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
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                                                                                                                                                                                                                                                                                                                                                                    PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                             66.4%; Score 3706.5; DB 2; Length 1181;
larity 65.4%; Pred. No. 2e-210;
Conservative 151; Mismatches 174; Indele 55;
                                                                                                                                                              ANK repeat; Hypothetical protein; Repeat.
SEQUENCE 1181 AA; 127885 MW; 4E2BF31549BBA2D9 CRC64;
InterPro; IPR002110; ANK.
InterPro; IPR001290; PARP.
InterPro; IPR001291; PARP—catalytic.
InterPro; IPR001660; SAM.
InterPro; IPR011510; SAM_2.
Ffam; PF00023; Ank; 17.
Pfam; PF00644; PARP; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00447; SAM_2; 1.
Pfam; PF00447; SAM_2; 1.
PRINTS; SM004249; ANK; 15.
SMART; SM004249; ANK; 15.
SMART; SM00454; SAM; 1.
PROSITE; PS50089; ANK_REPERT; 14.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTEGASSLEKKEVPGVD--FSIT
                                                                                                                                                                                                                                     QFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQG
                                                                                                                                                                                                                                                                                             LNPYLTLNTSGSG-----TILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       928 ILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
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OFFRB-2006, entry version 5.
Chromosome 4 SCAF14752, whole genome shotgun sequence. (Fragment)
ORFNames=GSTENG00024768001;
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NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-I- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA
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                                                                                                                                                                                                                Gaps
                                                                                                                                                                                    56.9%; Score 3179; DB 2; Length 1047;
59.1%; Pred. No. 3e-179;
tive 68; Mismatches 134; Indels 250;
GO:0006471; P:protein amino acid ADP-ribosylation; IEA
                                                                                                                                ANK repeat.
NON TER 1047 1047
SEQUENCE 1047 AA; 114477 WW; 09E9D3AE198C75E7 CRC64;
                                                                                                                                                                                                                                                                                                GADVHAKDKGDLVPLHNACSYGHYEVTELLVK-------
         InterPro; IPR002110; ANK.
InterPro; IPR012317; PARP_catalytic.
Pfam; PF00023; Ank; 13.
Pfam; PF00644; PARP; 1.
PRINTS; PR01415; ANKYRIN.
SMART; SM0248; ANK; 9.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50088; ANK REPEAT; 10.
PROSITE; PS51059; PARP_CATALYTIC; 1.
                                                                                                                                                                                     Query Match
Best Local Similarity 59.19
Matches 652; Conservative
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ò	THRRKEVSEE	95
Q	835RDDRPGSRRQGVPVCGGGAAEHHPRAPRWRERRRSLQPL 8	87
È	NHNHANÈRMLFHOSPFVNAIIHKGFDERHAYIGGMFGAFI	99
d d		93
È	994 YFAENSSKSNQYVYGIGGGTGCPVHKDRSCYICH	Ò
В		99
ò	1042 LQFSAMKWAHSPEGHHSVTGRPSV 1065	
අු	994	
RESULT Q3UES3 ID Q3	LT 15 83 MOUSE QJUBS3 MOUSE PRELIMINARY; PRT; 589 AA.	
SE!	Q3UES3; 11-OCT-2005, integrated into UniProtKB/TrEMBL.	
2 2 2	11-001-2005, Beguence Version 1. 07-FEB-2006, entry version R. Adult male liver tumor cDNA, RIKEN full-length enriched library,	
DE	clone:C730001F05 product:Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1- interacting ankyrin-related ADP-ribose polymerase	
8 B B	 (Tankyrase-like protein) (Tankyrase-related protein) nomolog (Fragment). 	
S S	Name=Tnk82; Mus musculus (Mouse).	
88	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
ខ្ព	Muroidea; Muridae; Murinae; Mus. NCBI_TaxID=10090;	
R R	[1] NUCLEOTIDE SEQUENCE.	
2 2 2 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4	STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	
RA	Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";	
R R	Methods Enzymol. 303:19-44(1999). [2]	
R P	NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Liver;	
X Z	PubMed=16141072; DOI=10.1126/science.1112014; Carninci P. Kasukawa T. Katayama S. Gough J. Frith M.C. Maeda N.	
Z Z	<u>.</u>	
12	Davis M.J., Wilming L.G., Aidinis V., Allen J.B.,	
\$ \$:	Ambesi implomeato A., Apweller K., Aturaliya K.N., Balley 1.E., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,	
8 8	Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.K., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,	
\$ \$	di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,	
R &	Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Havashi Y., Hensch T.K., Hirokawa N.,	
æ	Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,	
\$ \$ 1	Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,	
\$ \$	Kurocnkin 1.V., Lareau L.F., Lazarevic D., Lipovici L., Liu V., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,	
8 8	Matguda H., Matguzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottaqui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,	
RA 6	Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Oharati V., Orlando V., Dang K.C., Dayan W.T., Dayesi G., Pesole G.	
§ §	Okazaki I., Orlando V., Fang N.C., Favan M.U., Favesi G., Febole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,	

Refines B. Runn V. Saltaguch K., Semple C.A., Senos S., Sessa I., Sheng Y., Reinberg V., Shinada K., Shinada K., Shilara D., Shilara I. Shilara V., Taki K., Shilara R., Take M., Shilara V., Taki K., Shilara R., Takenaka Y., Taki K., Taka M., Taka M., Taka M., Taka M., Shilara R., Shilara R.

Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License STRAIN=C57BL/63; TISSUB-Liver;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."; Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Gaps Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori P., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. MEDLINE-20530913; PubMed=11076861, DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Saeaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishinc T., Tashiro H., Itoh W., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Cawa K., Tanaka T., Matsuura S., Kawai J., Nohara E., Watshiki M., Ohazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). E MBL; AK14936; BAE28038.1; -; mRNA.

R MGI; MGI:1921743; TING.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:000356; F:NAD+ ADP-ribosyltransferase activity; IEA.

R GO; GO:000471; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR001230; PARP.

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R PRINTS; SN00248; ANK; 1.

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US-11-371-354-5620

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US-10-533-519-1308

US-11-317-329-34

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114 YMAAQENHIDVVKYLLENGANQSTATEDGFTPLAVALQQGHNQAVAILLENDTKGKVRLP 173
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Sequence 3237, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIN Ver. 2.1
SOFTWARE: PatentIN Ver. 2.1
SENGTH: 1330
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US-11-293-697-3237
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Db 199 DVLSKTGFTPLHIAAHYENLNVAQLLLNRGASVNFTPQNGITPLHIASRR 248 Ov 156 NRVKIVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPL 215	249	Qy 216 HEAASKNRVEVCSLLLSYGADFTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAARE 275 : :	276 ADVTRIKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFL	Db 332 - DITDHLITPLHVAAHCGHHRVAKVLLDKGAKPNSRALNGF 371 Qy 336 TPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNI 395	Db 372 TPLHIACKUNHVRVMELLKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNV 431 Qy 396 ISLQGFTALQMGNENVQQLLQEGISLGNSEADRQLLE- 432	SINYKVETPLHMAARAGHTEVAKYLLQNKAKNAKAKDDQTPLHCAARIGHTNNVKLLLEN	OY 433ARKGDVETVKKLCTVQ-SVNCKDIEGKŲSTPLHFAGSIRKVS 474	VVEXILQHGADVHAKDKGGIVPLHNACSYGHYEVAELLVKHGAVVNVADLWK-FTPLHEA	Db 550 VAELLIERDAHPNAAGKNGLTPIHVAVHHNNLDIVKLLLERGGSPH-SFAWNGYIPLHIA 608 Qy 534 AAKGKYEICKLILQHGADPTKKNRDGNTPLDL-VKDGDTDIQDLIRGDAALLDAAKKGCL 592	609	DD 654LSKQANGNLGNKSGLTPLHLVAQBGHVPVADVLIKHGVMVDATTRMGYTPLHV 706	Qy 653 AASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEG 712	OY 713 QTPLDL748ADDVSALLTAAMPPSALPSC740 	Qy 741AASSLDN 777 CY 141AASSLDN 777 CY 15: : : : : : : : : : : : : : : :	977	Qy 838 LVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNFYLTLNTSG 884 Db 918VDARGGSMRGSRHNGLRVVIPPRTCAAPTRITCRLVKPQKLSTPPPLAEEEG 969 .			Db 1021 SRYGESYLDQILN 1033	RESULT 3 US-11-050-875-629 US-11-050-875-629 ; Sequence 629, Application US/11050875 ; Publication No. US20060263786A1 ; GENERAL INFORMATION: ; APPLICANT: Compugen Ltd
Qy 339 HVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISL 398	399 QGFTALQMGNENVQQLLQEGISLGNSEADRQLLE	Db 442 RGETALHWAARAGQVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHWAH 501	PDAATTNRYTPLHISAREGQVDVASVLLEAGAHSLATK-KGFTPLHVAAKYGSLDVAKL	Qy 479 ILQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHQAVNNVADLWKFTPLHEAAAKGK 538	Qy 539 YEICKLILQHGADPTKKNRDGNTPLDLV-KDGDTDIQDLLRGDAALLDAAKKGCLARVKK 597	598	Db 676TSLHLAAQEDKVNVADILTKHGADQDAHTKLGYTFLIVACHYG 718 Ov 658 HVDVAALLIKXNACVNATDKMAFTPLHEAAOKGRTOLCALLLAHGADPTLKNQEGQTPLD 717		Qy 718 LVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSA 771 :	772 ASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRN	DD 827 EEGDDTMTGDGGEYLRPEDLKELGDDSLPSSQFLDGMNYLRYSLEGGRSDSLRSFSSDRS 886 OV 819 LGLEHLMDIFERROITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERL 867	887 HTLSHASYLRDSAVMDDSVVIPSHQVSTLAKEAERNSYRLSWGTENL	RESULT 2 US-11-050-875-628 j. Sequence 629, Application US/11050875 j. Publication No. HS20060263786A1	; GENERAL INFORMATION: ; APPLICANT: Compugen Ltd ; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS ; TITLE OF INVENTION: THEREOF FOR DIAGNOSTS OF COLON CANCER		; SEQ ID NO 628 ; LENGTH: 1880 ; TYPE: PRT)50-875-628 / Match 15.1%; Score 842	Best_Local Matches 2		Qy 63 HEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKD 113

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828 KAERRDSRDVDEEKELLDFVPKLDQVVESPAI------PRIPCAMPETVVIRSEEQEQ 879
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                                                                                        LSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDV
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                                                                                                                                                                                                                                                                                                                                                                          971 IASRITALGPTGAQFLSPVIVEIPHFASHGRGDRELVVLRSENGSVWKEHR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 919;
                                                                                                                                 880 ASKEYDEDSLIPSSPATETSDNISPVASPVHTGFLVSFM-----
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Best Local Similarity 28.5%; Pred. No. 3.7e-35;
Matches 235; Conservative 109; Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL Full length CDNA FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
NUMBER OF SEQ ID NOS: 5528
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                LVEMGHKELKEIGINAYGHRHKLIKGVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4122, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRYGESYLDQILN 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 NRYNILKIQKVCN 936
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US-11-293-697-4122
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LENGTH: 919
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TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODE TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER FILE REFERENCE: 1847.1001 CURRENT APPLICATION NUMBER: US/11/050,875 CURRENT FILING DATE: 2005-01-27 NUMBER OF SEQ ID NOS: 1583 SEQ ID NOS: 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : | : | | | | AVALQQGHENVVAHLINYGTKGKVRLPALHIAARNDDTRTA------AVLLQNDPNP 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRVKIVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :|:|| || : | | : | || | | || GNVINVELLLDRGAQIETKTKDELTPLHCAARNGHVRISEIILIDHGAPIQAKTKNGLSPI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAASKNRVEVCSLLLSYGADPTLLNCHNKSALDLAPTPQLKERLAYEFKGHSLLQAARE 275
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US-11-050-875-629
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Sequence 1308, Application US/10533519

Publication No. US2060263774A1

Publication No. US2060263774A1

GENERAL INFORMATION:
APPLICANT: CLARK, HILARY

APPLICANT: VANLOOKERED, JILL
APPLICANT: WILLIAMS, P. MCKEY
APPLICANT: WILLIAMS, P. MCKEY

APPLICANT: WU, THOMAS D.

TITLE OF INVENTION: COMPOSITIONS AND METHODSF OR THE TREATMENT OF IMMUNE

TITLE OF INVENTION: RELATED DISEASES

TITLE OF INVENTION: RELATED DISEASES

TITLE OF INVENTION NUMBER: US/10/533,519

CURRENT APPLICATION NUMBER: US/10/533,519

CURRENT FILING DATE: 2005-04-28

PRIOR PPLICANTION NUMBER: US/03/34312

PRIOR PPLICATION NUMBER: US 60/423,394

PRIOR FILING DATE: 2002-11-01

WMMBER OF SEQ ID NOS: 2517

LENGTH: 685
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                               118 SARSGNEEKWWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKG 177
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9.4%; Score 527; DB 7; Length 743;
Best Local Similarity 24.0%; Pred. No. 1.3e-25;
Matches 201; Conservative 98; Mismatches 238; Indels 302;
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US-11-371-354-56501
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Publication No. US20060105413A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
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119 VSIACAGGHLAVVELLLAHGA------DPTHRLKDGSTMLIEAAKGGHTNVVSYLL 168
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
; ORGANISM: Homo sapien
US-10-533-519-1308
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APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Innchara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling.
FITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling.
FILE REPERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR PILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 3-4
LENGTH: 765
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                                                                                                                                                                                                                                           Length 765;
                                                                                                                                                                                                                                     Query Match 8.3%; Score 465; DB 7; Length 76 Best Local Similarity 30.1%; Pred. No. 1.3e-21; Matches 144; Conservative 65; Mismatches 181; Indels
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Publication No. US20060105413A1
GENERAL INFORMATION:
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                      NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 3:
LENGTH: 765
PRIOR FILING DATE: 2002-04-23
                                                                                                                                                          ORGANISM: Homo sapiens
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Sequence 36, Application US/11317329
Sequence 36, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-05967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
RROR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 765
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Matches 144; Conservative
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US-11-317-329-36
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APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Machiro
TILE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION WINBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NUMBER: US/10/128,174
SURING APPLICATION NUMBER: US/10/128,174
SOFTWARE: Patentin version 3.1
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                                                                                                                                                              Query Match

8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels
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                                                                                         387 DVDCQTASGY-----
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US-11-317-329-35
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SEQ ID NO 38
LENGTH: 765
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LENGTH: 765
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                                                            GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Nunez, Gabriel

APPLICANT: Nunez, Machico

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR PILING DATE: 2005-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.1

SEQ ID NO 37

LENGTH: 765
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APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Inhorara, Naobiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
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Publication No. US20060105413A1
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Publication No. US20060105413A1
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Matches 144; Conservative
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                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-11-317-329-37
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Sequence 39, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
BAPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
CURRENT APPLICATION WIMBER: US/11/317,329
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30.1%; Pred. No. 1.3e-21;
iive 65; Mismatches 181; Indels 8
                                                                                                                                                                                            8.3%; Score 465; DB 7; Length 765; 30.1%; Pred. No. 1.3e-21;
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PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
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Matches 144; Conservative
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Matches 144; Conservative
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NG-11-317-329-41

Sequence 41, Application US/11317329

Sequence 41, Application WS/11317329

Publication No. US20060105413A1

SEQUENCE AND THE NEW PROBLEM TON:

APPLICANT: Numez, Gabriel

APPLICANT: Numez, Gabriel

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT PELICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: 2005-04-23

NUMBER OF SEQ ID NOS: 44

SCOTWARE: Patentin version 3.1
                                                                                                                                                               245 KSAIDLAP----TPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300
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                      541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600
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Sequence 40, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inchara, Nachiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

PILE REPERENCE: UM-06.67

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR APPLICANT UNUMBER: US/10/128,174

PRIOR PILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.1

LENGTH: 765
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                               -----TPLLIAAQDQQPDLCALLLAHGADA 421
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8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels
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ORGANISM: Homo sapiens
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(without alignments) 3489.682 Million cell updates/sec

US-10-616-101-4

6464 1 RCSARRGAAGGQGAQRGARV.....AYPEYLITYQIMRPEGMYDG 1240 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 seqs, 457216429 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* A_Geneseq_8:* 1: geneseqp19 **Database**:

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*, geneseqp2003as:* geneseqp2003bs:* geneseqp2006s:* geneseqp2004s:* geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-		Description	Aay97749 Tankyrase	Abg73731 Tankyrase	Adh69406 Human tan	Ady97762 Human tan	Aab66290 Human tan	Adr66429 Human pro	Adr66087 Human pro	Aab66294 Human tan	Aab66288 Human tan	Aab66278 Human tan	Aab66295 Human tan	Adr14792 Amino aci	Aab27211 Human tan	Abp69457 Human pol	Aay72589 Human tan	Aay97748 Tankyrase	Abg73732 Tankyrase	Abg73730 Tankyrase	Adh69405 Human tan	Ady97766 Human tan	Abg73735 Tankyrase	Ady97769 Human tan	Abg73736 Tankyrase
		ID	AAY97749	ABG73731	ADH69406	ADY97762	AAB66290	ADR66429	ADR66087	AAB66294	AAB66288	AAB66278 .	AAB66295	ADR14792	AAB27211	ABP69457	AAY72589	AAY97748	ABG73732	ABG73730	ADH69405	ADY97766	ABG73735	ADY97769	ABG73736
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Ady97770 Human tan	Aay05734 Human Grb	Ady97761 Human tan	Aab47022 Human SPA	Aab27210 Human tan	Aae35352 Human col	Aay44402 Human tan		Aab66279 Human tan		Adr14791 Amino aci	Aab27209 Human tan		Aab48574 Human bre	Aab66285 Human tan	Abb60894 Drosophil	Aab66297 Drosophil	Aab66286 Human tan	Aao20512 Protein o	Aay44404 Human tru	Aau79539 Truncated	Ady97768 Human tan
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87.5	86.7	86.4	85.8	84.7	82.0	79.0	79.0	79.0	79.0	79.0	78.0	77.9	71.5	63.5	62.0	61.8	61.2	6.09	51.2	51.2	45.1
5656	5605	5582	5543	5474	5303.5	5103.5	5103.5	5103.5	5103.5	5103.5	5040.5	5038.5	4624.5	4102	4005	3997	3959	3938	3307	3307	2913
24	25	56	27	58	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY97749

AAY97749 standard; protein; 1240 AA.

AAY97749;

06-AUG-2001 (first entry)

Tankyrase homologue isotype 2 protein sequence

Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation; cell cycle protein; cell cycle associated disorder; cancer; gene mapping; chromosome mapping; gene therapy; vaccine.

Unidentified.

WO200130987-A2.

03-MAY-2001.

25-OCT-2000; 2000WO-US041528

99US-00427154 25-OCT-1999;

(RIGE-) RIGEL PHARM INC

Χu Χ, Chan E, Luo Y,

Huang B;

WPI; 2001-300503/31. N-PSDB; AAA91488.

Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer.

Claim 22; Fig 4; 63pp; English.

This sequence is the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-2 protein. The TaHo proteins are useful for inducting or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are useful for the preparation of TaHo, for generating either transgenic

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animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with genetic disorders. The TaHo proteins, and their coding sequences are
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100.0%; Score 6464; DB 4; Length 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 0; Indels 0;
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1080 1080 1140 1200 1020 Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2; TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour; cell cycle related disorder; poly ADP-ribose polymerase; PARP. This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a tumour cell. The methods are useful for screening for a bloactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or PARP (pply ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents the tankyrase H isoform 2, TaHo-2, isolated from for ERYTHRRKEVSEENHINHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS KSNOYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVT SGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLG SGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLG LEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTL NTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLW ERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS useful i cycle protein, disorder, e.g. GRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240 Tankyrase H isotype 2 TaHo-2 fragment from clone K23. New recombinant nucleic acid encoding a cell diagnosing and treating a cell cycle related В, Оввоувкауа Z ABG73731 standard; protein; 1240 Claim 14; Fig 4; 90pp; English Chan E, Xu X, Huang 25-APR-2002; 2002WO-US013185 25-APR-2001; 2001US-00843159 (first entry) (RIGE-) RIGEL PHARM INC WPI; 2003-093158/08. N-PSDB; ABQ77067. WO200286170-A1. 08-APR-2003 31-OCT-2002 1021 1021 1081 1081 1141 1141 901 961 1201 901 961 1201 Luo Y, RESULT 2 ABG73731 셤 ઠે g ઠે g ð 셤 8 g ଚ

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bioactive agent screening; cancer; cytostatic;
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ive 0; Mismatches
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Matches 1240; Conservative
 clone K23 which is
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1021 NTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLW
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25-APR-2001; 2001US-00843159.
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The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (TaHo), comprising an amino acid sequence having 85% or more sequence identity to the 1065 amino acid sequence having 85% or more sequence identity to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (1) diagnosing cancer, which involves determining the activity of (I) from a test sample of an individual and individual with a cell cycle control with a control; (2) treating (M1) an individual with a cell cycle related disorder, which involves administering to the individual an inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (II).

CC related disorder, which involves administering to the individual an inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (II).

CC comprising a nucleic acid that hybridizes under high servingent confidence of ADY97759 or a nucleic acid having 85% or the 3816 base pair sequence of ADY97759, or a nucleic acid having 85% or comprising (II) operably linked to regulatory sequences recognized by a host cell (IV) transformed with the nucleic acid; (5) a host cell (C); and sequence identity to ADY97759 or ADY97760; (4) an expression vector (III) comprising (II) or (III); (6) producing (I); (7) a polypeptide that specifically binds to (I); and (8) inhibiting divalence contacting the tumor with a bloactive agent capable of inhibiting TaHo activity. (I) is useful for screening a bioactive agent capable of interfering with the binding of (I) and P21. (M1) is useful for treating an individual with a cell cycle related disorder. (M2) is useful for individual with a cell cycle related disorder. (M2) is useful for inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
1141 KSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVT 1200
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                                                                                                                       1 RCSARRGAAGGÓGAQRGARVGAAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLL
                                                                                Gaps
   present sequence represents the human tankyrase
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                                                         Length 1240;
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                                                         DB 9;
                                                         Score 6464;
Pred. No. 0;
0; Mismatches
                                                        100.0%;
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Best Local Similarity 100.
Matches 1240; Conservative
oligonucleotide. The
              homologue isotype 2.
                                   Sequence 1240 AA;
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961 LEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTL 1020
                                                                                                      NTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLW 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mediated by cancers,
                                                                                                                                                                                                             ERYTHREKEVSEENHWHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS
                                                                                                                                                                                                                                                                                     KSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVT
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                                                                        NTSGSGT1L1DLSPDDKEFQSVEEEMQSTVREHRDGGHAGG1FNRYN1LK1QKVCNKKLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory and autoimmune disorders.
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Best Local Similarity 99.2
Matches 1225; Conservative
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                                                                                                                                                       ADR66429 standard; protein; 1287
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14-MAY-2003; 2003DE-01022134.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE), ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
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ROSENTHAL A.
HERMANN K.
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This invention describes novel cytostatic polymucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, contrarefering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptendar against the polypeptide; an organic molecule of molecular preferably humanised or human; an anti-idictype, non-human catanished, preferably humanised or human; an anti-idictype, non-human polypeptide, and are reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic ancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from
VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSV 1205
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Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
                                                                        VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV
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prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66554 represent the polymucleotide and polypeptide sequences used in the method of the
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         PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM
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, Bruemmendorf T, Kinnemann H, Roepcke S;
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14-MAY-2003; 2003DE-01022134.
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Beckmann (
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ROSENTHAL A.
HERMANN K.
PILARSKY C.
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corrections over transcription or ver expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences in prostatic tissue. Screening for inhibitors of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polymeptide; an aptamer against the polymeptide; a (monoclonal) antibody (Ab) against the colymeptide, preferably humanised or human; an anti-idotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated second antibody; streptavidin-conjugated horseradish percentially with anti-human CD4 murine monoclonal antibodies; blocking become antibody; streptavidin-conjugated horseradish cancer patients, or subjects at risk, were incubated second antibodies; become antibodies; strongly but non-mailignant cells only weakly. In 15 of 51 samples were counterstained with hemalum (blue). Malignant cells stained sequenced by many one metalignant cells only weakly. In 15 of 53 samples of adenocacinoma, membrane and cytoplasmic staining was very strong, and incoming polymucleotide and polypeptide sequences used in the method of the developing prostatic cancer. Diagnosis is based on 88888888888888888888888888888888888

Sequence 1287 AA;

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305 172 232 245 292 425 413 VCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHL 472 485 532 545 605 LLAVAAARIMSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNS 125 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLL 185 LTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 352 306 QHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVE 365 MGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH SLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKA HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQ RHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAV HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDNIISLQGFTALQ RGAAGGQGAQRGARVGAAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLAL RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLL RHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAV LTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL VCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHL SLEMVNPKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKA Gaps ä DB 8; Length 1287; 8; Indels 98.6%; Score 6375.5; 99.2%; Pred. No. 0; 1; Mismatches Best Local Similarity 99.2 Matches 1225; Conservative 113 293 ø 99 173 233 Query Match 186 246 353 366 426 486 533 546

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1085 1025 1072 725 785 845 892 905 952 965 832 593 MGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 652 1013 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGS GTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTH VYGIGGGTGCPVHKDRSCYICHRQLLPCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1193 VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLW KFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLD KFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLD **AAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG** GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADP TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM GTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTH RRKEVSBENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQY DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGS Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging; Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL; 1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240 Human tankyrase2 TANK2-LONG SEQ ID NO: 133 AAB66294 standard; protein; 1385 28-JUN-2000; 2000WO-US017827 (first entry) inflammatory disorder WO200100849-A1 Homo sapiens. SODI (-SODI) 29-JUN-1999; 05-APR-2001 04-JAN-2001 846 999 893 953 996 1073 1086 1146 713 773 786 906 1026 726 RESULT 8 셤 셤 g ઠે 셤 õ Вþ ઠ g ઠે 셤 ઠ 셤 ઠે 유 ò 유 ò ò ò ઠ

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                          PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM
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                                                                                                                                                                                                          The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRP1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory
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                                                                                  New tankyrase2 polypeptides, useful for treating conditions mediated poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders.
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                                                                                                                                                                    Claim 2; Page 191-194; 242pp; English
                        WPI; 2001-102896/11
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                                          N-PSDB; AAF63952
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The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding procein. The regulation of telomere length, in which TRF1 has a role, is linked to against and cancer. The sequences are useful in the treatment of cancers and inflammatory
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                                                  EYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240
                                                                 Human tankyrase2 TANK2-SHORT SEQ ID NO:
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                            KSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to againg and cancer. The sequences are useful in the treatment of cancers and inflammatory
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Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
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                                            DKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYG
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ADR14792 standard; protein; 1166 AA.

RESULT 12 ADR14792 ADR14792

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The specification describes a method for identifying a candidate

adenomatous polyposis coli protein (APC) and axin pathways modulating

agents. The method comprises providing an assay system comprising a

modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting

confider of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting

the assay system with a test agent, the system provides a reference acitivity, and

detecting a test agent. biased activity of the assay system, where a

difference between the test agent as a candidate APC and axin pathways

contivity identifies the method is useful in identifying a candidate

adenomatous polyposis coli protein (APC) and a pathways modulating agent,

which are useful for preparing a composition for diagnosing or treating

cancer. The present sequence represents a human orthologue of a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a candidate adenomatous polyposis coli protein (APC) and axin pathways modulating agent for treating cancer by contacting an assay system comprising a modifier of APC and axin polypeptide or nucleic acid with a test agent.
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                                                              Amino acid sequence of human MAPCAX orthologue #24.
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11.FEB-2003; 2003US-0447358P.
10-APR-2003; 2003US-046189P.
14.MAY-2003; 2003US-0470664P.
19-JUN-2003; 2003US-0479650P.
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Best Local Similarity 100.
Matches 1166; Conservative
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protein;

standard;

AAB27211

AAB27211

(first entry)

27-FEB-2001

AAB27211;

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The present sequence is a version of the human tankyrase II protein sequence. The protein is thought to be involved in signal transduction in the cell, and to have binding activity for other telomere-associated proteins. It is possible that it plays a role in the regulation of telomere length, thus affecting the replicative ability of the cell. The protein is useful for ribosylating target proteins, for determining tankyrase II binding activity in a sample, and for modulating telomere
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                                       Human; tankyrase II; telomere length; signal transduction.
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99.8%; Pred. No. 0;
cive 0; Mismatches 2;
            ö
            Human tankyrase II protein sequence SEQ ID
                                                                                                                            'note= "encoded by TTA"
                                                                                                                                                        /note= "encoded by TAC"
                                                                                                Location/Qualifiers
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N-PSDB; AAC66825.
                                                                                                                                            Misc-difference 125
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                                                                                                              Misc-difference
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                PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVV
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PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVV
                                                      KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQL
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Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease, Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;

Human polypeptide SEQ ID NO 1504

XUXHXMXXXXXXX

(first entry)

20-JAN-2003

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The invention relates to an isolated polymucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-CABZ1066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polymucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers as a food supplement, for generating antibodies, in medical mapping, screening and diagnostic assays and for treating cell-captive diseases (antiple sclerosis, corpliferative diseases (antiple sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parastic), arthritis, etc. Note: The sequence data for this patent did not form part directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 1504; 1012pp + Sequence Listing; English
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R, Wang 2
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Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R,
Wehrman T, Wang J, Wang D, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or coagulation disorders.
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                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                        antiarthritic.
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                                                      PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVV
                                                                                                KHEAKVNALDNIGGTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQL
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                                          PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVV
                                                                                     KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQL
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The present sequence is human tankyrase homolog protein (THP). The THP polypeptides and polymucleotides of the invention are useful in gene therapy and for treating or preventing unregulated cell growth such as cancer or tumour (e.g. basal cell carcinoma). The nucleic acid molecules of the invention and their fragments are useful for restriction fragment length polymorphism (RFLP) associated with certain disorders, as well as for genetic mapping. Antisense oligomucleotides, or fragments of nucleic acid encoding THP are useful as diagnostic tools for probing the expression of Thp gene in various tissues. THP can be used as antigens for raising antibodies against them and in assays for identifying compounds that modulate their activity. They are used in the manufacture of a medicament directed towards cancers or tumours. THP are also useful for screening compounds in a variety of drugs screening techniques and as a research tool for identification, characterisation and purification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tankyrase homolog protein (THP) polynucleotide and polypeptide useful in gene therapy, diagnosis and treatment or prevention of unregulated cell growth, such as cancer or tumor cell growth.
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Human, tankyrase homolog protein; THP; gene therapy, cancer; tumour; basal cell carcinoma; therapy; genetic mapping; cytostatic.

tankyrase homolog protein (THP)

(first entry)

02-MAY-2001

AAY72589

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AAY72589 standard; protein; 1166

AAY72589

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- protein search, using sw model OM protein

; Search time 153.857 Seconds December 18, 2006, 17:51:56 Run on:

(without alignments) 3733.253 Million cell updates/sec

US-10-616-101-4

Title: Perfect score:

6464 1 RCSARRGAAGGQGAQRGARV.....AYPEYLITYQIMRPEGMYDG 1240 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

2097797 segs, 463214858 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*/EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*/ Published_Applications_AA_Main:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description Sequence 30. -10-199-937-107 V SUMMARIES Query Match Length DB 6464 6375.5 6375.5 6121 6121 6108 6108 6108 5877 5766 5103.5 5103.5 5103.5 5031.5 4102 4005 3997 3959 3938 3938 Score

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Sequence 4, Application US/10616101
Publication No. US20050074825A1
GENERAL INFORMATION:
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US-10-199-937-107
Sequence 107, Application US/10199937
Sequence 107, Application US/10199937
Sequence 107, Application US/10199937
September 100 US/10199937
APPLICANT: Christenson, Erik

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APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: Goldman, Phyllis S.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND MET
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR APPLICATION NUMBER: GO/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 107
LENGTH. 1262
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99.2%; Pred. No. 0;
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Best Local Similarity 99.2
Matches 1225, Conservative
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CRGANISM: Homo sapiens
US-10-199-937-107
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                          PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM
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                                                                           TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS
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Sequence 133, Application U9/10199937

Sublication No. US20030190739A1

GENERAL INFORMATION:

APPLICANT: Christenson, Erik
APPLICANT: Goldman, Phyllis S.

APPLICANT: Goldman, Phyllis S.

TITLE OF INVENTION: TANKTRASEZ MATERIALS AND METHODS
FILE REFERENCE: 27866/3659

CURRENT APPLICATION NUMBER: US/10/199,937

CURRENT APPLICATION NUMBER: US/09/606,035

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 178

SOFTWARE PATENTIN VET. 2.0
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Pred. No. 0;
1; Mismatches
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1225; Conserv
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LENGTH: 1385
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                                                                            LARVKKLSSPDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLH
                                                                                                                            NAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQE
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APPLICANT: Goldman, Phyllis S.
APPLICANT: Goldman, Phyllis S.
TITLE OF INTEXTION: TANKTRAEZ MATERIALS AND METHODS
FILE REFERENCE: 27866/3659
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches
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SEQ ID NO 101
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US-10-199-937-101
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                                                                                  **Sequence 2, Application US/1019937;
**Publication No. US203019073941
**GENERAL INFORMATION:
**APPLICANT: Christenson, Erik
**APPLICANT: DeMaggio, Anthony J.
**APPLICANT: Goldman, PNY11s S.
**APPLICANT: Goldman, PNY11s S.
**APPLICANT: Goldman, PNY11s S.
**APPLICANT: Goldman, PNY11s S.
**APPLICANT: Goldman, PNY11s S.
**APPLICANT: Goldman, PNY11s S.
**APPLICANT: WEBLISCE, US/10/199,937
CURRENT APPLICATION NUMBER: US/09/606,035
**PRIOR APPLICATION NUMBER: US/09/606,035
**PRIOR PILING DATE: 2000-06-29
**PRIOR PILING DATE: 1999-06-29
**NUMBER: OF SEQ ID NOS: 178
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       1351 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1385
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100.0%; Pred. No. 0;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1169; Conservative
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ORGANISM: Homo sapiens
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                                                                 US-09-972-115A-6

Sequence 6, Application US/09972115A

Sequence 6, Application US/09972115A

Publication No. US20030032769A1

GENERAL IMPORMATION:

APPLICANT: Greeg, Morin B.

APPLICANT: Walter Funk D.

TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/03C

CURRENT PAPLICATION NUMBER: US/09/972,115A

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 60/128,577

PRIOR APPLICATION NUMBER: US 60/129,123

PRIOR FILING DATE: 2000-04-10

PRIOR FILING DATE: 2000-04-10

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 6
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1141 EYVIYRGEQAYPEYLITYQIMRPEGWVDG 1169
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94.5%; Score 6108; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches
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                      SYGHVDVAALLIKYNACVNATDKWAPTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQT
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Publication No. US20030165834A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REPERENCE: L0461/7105(RN)
CURRENT FILING DATE: 2001-05-04
CURRENT FILING DATE: 2001-05-04
CURRENT FILING DATE: 2001-05-04
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Matches 1148; Conservative
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                            Sequence 135, Application US/1019937

Publication No. US2003019073941

GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: Goldman, Phyllis S.
TITLE OF INVENTION: TANKTRASE MATERIALS AND METHODS
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US/09/606,035

PRIOR PRILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-29

PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 178

SOFTWARE: Patentin Ver. 2.0
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94.5%; Score 6108; DB 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                    US-10-199-937-135
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yethlicant: Luo, Ying
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89.2%; Score 5766; L

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1099; Conservative 1; Mismatches CREANISM: Homo sapiens US-10-616-101-8

Db 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60		Oy 261 SGNEEKWMALLTPLNVNCHASDGEKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV	Qy 321 PLHNACSYGHYBUTELLVKHGACVNAMDLWQFTFLHBAASKNRVBVCSLLLSYGADPTLL	DD 181 PLHNACSYGHYEVTELLVKHGACVNAMDLWGFTPLHEAASKNRVEVCSLLLSYGADFTLL Qy 381 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAARBADVTRIKKHLSLEMVNFKHPQTHBT	Db 241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 30 441 ALHCAAASPYPKRKOICELLLRKKGANINEKTKEFLTPLHVASEKAHNDVVEVVKHEAKV 50	301 ALHCAAASPYPKRKQICELLLRKGANINBKTKBFLTPLHVASBKAHNDVVBVVVKHEAKV	Qy 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS Db 341 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS	561 LGNS	Db 421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480 Qy 621 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 680	DD 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE	QY 681 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740	QY 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800 Db 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660	801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADFTLKNQEGQTPLDLVS	OY 861 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 920	921	Qy 981 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 104	Qy 1041 SVBEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLMERYTHRRKEVSEENHNHANE 1100 DD 901 SVBEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLMERYTHRRKEVSEENHNHANE 960	Qy 1101 RMLFHGSPFVNAIJHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1160 Dh	1161 RSCYICHROLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSVNGLALABYVIYRGEQ 1161 RSCYICHROLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSVNGLALABYVIYRGEQ 1021 RSCYICHROLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSVNGLALABEVVIYRGED	1221 AYPEYLITYQIMEPEGMVDG 1240
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Sequence 2, Application US/09509196A
Sequence 3, Application Sequence
APPLICANT: DALY, Roger J.
APPLICANT: SUTHERLAND, Robert L.
TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
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                                                                             PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLI PLHNAASYGHVD
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SOFTWARE: Patentin Ver.
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APPLICANT: Luo, Ying
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Worker Sector
APPLICANT: Ossovakaya, Valeria
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILER REFERENCE: RIGL-0107(19)
FILER REFERENCE: RIGL-0107(19)
CURRENT APPLICATION NUMBER: US/10/616,101
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR PILING DATE: 1000-10-25
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SED ID NO 12
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                                                                                                  Sequence 12, Application US/10616101
Publication No. US20050074825A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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APPLICANT: Luo, Ying
APPLICANT: Chan, Bva
APPLICANT: Chan, Bva
APPLICANT: Chan, Bva
APPLICANT: Chan, Bety
APPLICANT: Huang, Betty
APPLICANT: Ossovakaya, Valeria
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods of INTER OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods of INTER OF INTERIOR DIATE: 2003-07-08
FRIOR FILING DATE: 2001-04-25
FRIOR APPLICATION NUMBER: US 09/696,668
FRIOR FILING DATE: 2000-10-25
FRIOR APPLICATION NUMBER: US 09/427,154
FRIOR APPLICATION DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                            86.4%; Score 5582; Dilarity 99.9%; Pred. No. 0; Conservative 1; Mismatches
                                                                                                                                                          SOFTWARE: Patentin version 3.1 SEQ ID NO 3
                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-616-101-3
                                                                                                                                                                                                                                       Similarity
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Best Local Simil
Matches 1064; C
                                                                                                                                                                              LENGTH: 1065
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                                                                       MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKG
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ö 800 560 260 120 320 180 380 240 440 300 500 360 420 620 480 680 540 740 9 999 860 9 141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWYYT 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT SGNEEKMALLIPLINNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV PLHNACSYGHYEVTELLVKHGACYNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL NCHNKSAI DLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKGHLSLEMVNPKHPQTHET NALDNIGGTSLHRAAYGGHLQTCRLLLSYGCDDNIISLQGFTALQMGNENVQQLLQEGIS VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET ICKLILLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS Gaps ö Length 1065; Indels 2; ô 8 741 601 801 8 요 ð

US-10-616-101-3; Sequence 3, Application US/10616101; Publication No. US20050074825A1; GENERAL INFORMATION:

RESULT 14

Ser, Thr, Ile, Asp, or Phe. Asp, Gln, or Cys. or Leu. or Phe. or Leu. 'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys or Ser. or Tyr. or Tyr or Leu or Tyr. or Phe or Ile LOCATION: (741)..(741) OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu. 'Xaa' at location 215 stands for Lys, Asn, Glu, stop codon, or Tyr. 'Xaa' at location 227 stands for His, Arg, Pro, at location 188 stands for Asn, Asp, His, at location 205 stands for Asn, Ser, Thr, Hi8, 'Xaa' at location 667 stands for Tyr, Cys, Ser, 'Xaa' at location 727 stands for His, Arg, Pro, at location 173 stands for Ile, Val, Leu, at location 211 stands for Gln, Arg, Pro, 'Xaa' at location 213 stands for Ser, Gly, Arg, 'Xaa' at location 228 stands for Asn, Asp, His, at location 185 stands for Thr, Ala, Pro, NAME/KEY: misc_feature LOCATION: (237). (237) OCHER INFORMATION: The 'Xaa' at location 237 stands for Glu, or Asp. NAME/KEY: misc_feature LOCATION: (238). (238) OCHER INFORMATION: The 'Xaa' at location 238 stands for Asn, Ser, Th OCHER INFORMATION: Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe. 'Xaa' at location 725 stands for Lys, or Asn. or Lys 'Xaa' at location 202 stands for His, or Pro 'Xaa' at location 204 stands for Glu, or Lys 'Xaa' at location 735 stands for Glu, or Asp at location 207 stands for Asn, Asp, at location 174 stands for Glu, Val 'Xaa' at location 144 stands for Thr 'Xaa' at location 153 stands for Thr at location 183 stands for 'Xaa' 'Xaa' 'Xaa' 'Xaa' 'Xaa' 'Xaa' 'Xaa' 'Xaa' OTHER INFORMATION: The 'NAME/KEY: misc feature LOCATION: (725)...(725) NAME/KEY: misc feature
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NAME/KEY: misc feature
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LOCATION: (1667...(166)
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NAME/KEY: misc feature
LOCATION: (177)...(173) LOCATION: (1737...(173)
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NAME/KEY: misc feature
LOCATION: (1747...(174)
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NAME/KEY: misc feature
LOCATION: (1837...(183)
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LOCATION: (1857...(185)
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LOCATION: (188)...(188) LOCATION: (725)..(725) OTHER INFORMATION: The LOCATION: (727)..(727) OTHER INFORMATION: The LOCATION: (735)..(735) OTHER INFORMATION: The NAME/KEY: misc_feature NAME/KEY: misc feature LOCATION: (667)..(667) NAME/KEY: misc feature LOCATION: (727)..(727)

His

Gly

OCCATION: (781). (783). (781). (783). (781).	OTHER INFORMATION: The 'Xaa' at location 800 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Trp, Cys, or Phe. LOCATION: (801) - (801) OTHER INFORMATION: The 'Xaa' at location 801 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: Tyr, Trp, Cys, or Phe. NAME/KEY: misc feature LOCATION: (802) - (802) OHER INFORMATION: B4.3\$; Score 5452; DB 3; Length 1267;	Best Local Similarity 86.2%; Pred. No. Matches 1072; Conservative 6; Mismatches 1072; Conservative 6; Mismatches 1072; Conservative 6; Mismatches 1	121 EKVNSRDTAGRKGTPLHFAAGFCRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEV 180 [301 VOLLLOHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAAS 360 326 VOLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAAS 385 361 KNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTR 420	481 ASEKAHNDVVEVVVKHEAKVNALDNLGGTSLHRAAYGGHLGTCRLLLSYGCDPNIISLOG	661 VADLWKFTPLHEAAKGKYEICKLLLOHGADPTKKORRGNTPLDLVKGOTDIODLIRGD 720
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1137
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                                                                                              1021 NTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNK--- 1077
                                                                                                                                                925 SGPSSPSSLSAASSLDNLSGSFSELSSVVSSGGTEGASSLEKKEVPGVDFSITQFVRNLG 984
 965 XXXXXXXXXXXXXXXXXXXXXXXXXTAAMPPSVLPSCNKPQVLNGVRSPGATADALS 924
                  SGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLG
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Search completed: December 18, 2006, 17:59:55 Job time : 158.857 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

December 18, 2006, 17:27:10 ; Search time 38.1952 Seconds (without alignments) 3123.657 Million cell updates/sec Run on:

US-10-616-101-4 6464 1 RCSARRGAAGGQGAQRGARV.....AYPEYLITYQIMRPEGMVDG 1240 Title: .Perfect score: ,Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ankyrin 3, splice	'n	m	3, splic	'n	ť	ankyrin 1, erythro	ankyrin 1, erythro	۲,	ankyrin, erythrocy		ankyrin - fruit fl	ankyrin-related un	hypothetical prote	probable ankyrin	alpha-latroinsecto	ankyrin-like prote	inversin - mouse	Inv protein - mous	. alpha-latrotoxin p	hypothetical prote		_	24	hypothetical prote				hypothetical prote
SUMMARIES	CI	T42714	T42716	A55575	T42713	T42715	B35049	A35049	SJHUK	S37431	837771	I49502	T13940	T15347	T42691	H71274	S30355	D82654	T30255	T14151	S11527	T19552	AE2149	T25412	T00253	T24158	T24157	44	34	T46507
	DB	7	7	~	~	N	~	~	Н	7	7	N	7	~	N	н	7	7	7	7	~	~	~	7	~	~	~	~	7	7
	Length	1765	1961	4377	1943	1940	1856	1880	1881	3924	1848	1862	1549	2039	791	934	1411	1058	1062	1062	1401	1188	426	991	1184	2584	2606	397	1031	557
d	Query Match	13.8			13.8	13.		13.6	13.6	13.6		13.5	13.4	13.3	10.2	8.7	8.5	7.9	7.7	7.6	7.5	7.2	7.0	9.9	6.4	6.2	6.2		5.7	5.4
	Score	895	895	892.5	891	889	880.5	880.5	878.5	877	876	874	866.5	828	657	563.5	552	507.5	494.5	489.5	485	463	452.5	426	416.5	399	σ	389.5	370	350
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360 SKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVT 419

293 RSGHEQVVEMLLDRSA-PILSKTKN------

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hypothetical prote death-associated p	hypothetical prot	hypothetical prote	hypothetical prot	sex-determining p	myosin-light-chai	ankyrin related p	myosin heavy chai	2-5A-dependent RN	hypothetical prot	probable ankyrin	G9a protein - hum	hypothetical prote	transcription fac	protein phosphatas
AC2508	T21280	T32930	T21884	A34793	A55142	T19006	A59288	B45771	T27499	D84448	S30385	T21720	A42024	S68418
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606	1107	1435	1398	959	1004	1016	1322	619	633	247	1001	1295	900	658
0. 0.	5.3	5.1	5.0	4.9	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.4
348.5	343	329.5	321	315.5	. 307	306	306	305	299.5	299	297	297	294.5	285.5
30	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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329 ----HLNCVQLLLQHNVPVDDVTNDYLTALHVAAHCGHYK---VAKVLLDKKASPNAKAL 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 L-VKDGDTDIQDLL------RGDAALLDAAKKGCLARVKKLSSPD-NVNCRDTQ 750
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                                                                                   128 TAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRH 187
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-----VDVNICN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 RSGHEQVVEMLLDRSA-PILSKTKN---------GLSPLHMATQGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 RIKKHLSLEMVNFKH------PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     586 CTV-QSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 HYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLD
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                                                                                                                      55 QNGLNA--LHLASKEGHVEVVSELLQREANVDAATKKGNTALHIASLAGQAEVVKVLVTN
                                                                                                                                                                                              188 GADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLA----DPSA
                                                                                                                                                                                                                                                                                                            243 KAVLTGEYK---KDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVK
                                                                                                                                                                                                                                                                                                                                                                173 SLLLENDTKGKVRLPALHIAARKDDTKAAALLLQNDTNADVESKSGFTPLHIAAHYGNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNIISLOGFTALOMG-----NENVQQLLQEGISLGNSEADRQ--LLEAAKAGDVETVKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    811 CVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS-----ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 VSALLTAAMPPSALPSCYK---PQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLS-
                                                                                                                                                                                                                                                                                                                                                                                                                     300 IVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 EFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNA
10 AKPAHRKRKGKKSDANASYLRAARAGHLEKA----LDYIKNG-
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N;Alternate names: ankyrin G
C;Species: Homo sapiens (man)
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384 YLGPQDLKELG 894
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: T4216
R; Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.C. [1] Biol. 130, 313-330, 1995
A; Titls: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
A; Reference number: Z22237; MUID:95340633; PMID:7615634
A; Accession: T42716
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MINROT:061307; UNIPARC:UPI0000027D39; EMBL:L40632; NID:g710548; PIC
A; Experimental source: strain C57BL/6J; kidney
                                                                                                                                                                                                                                                                                                                                            644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLEVASLLLQKSASPDAAGKSGLTPLHVAAHYDNQKVALLLLDQGASPHAAAKNGYTPLH 619
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                                                                                                                   EPLIPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCD
                                                                                                                                                CTV-QSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYG
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                                                                                                                                                                                                                              PNIISLQGFTALQMG-----NENVQQLLQEGISLGNSEADRQ--LLEAAKAGDVETVKKL
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13.8%; Score 895; DB 2; Length 1961;
Best Local Similarity 30.3%; Pred. No. 3.3e-46;
Matches 294; Conservative 134; Mismatches 409; Indels 134;
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C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
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884 YLGPQDLKELG 894
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A, Description: supposed to play an important role in the polarized distribution of many 1 A, Note: major kidney ankyrin
A, Note: major kidney ankyrin
C; Superfamily: ankyrin, ankyrin, repeat homology
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T42713 K.M.; Lu, F.M.; Bicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L. S;Peters, LL.; John, K.M.; Lu, F.M.; Bicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L. J. Cell Biol. 130, 313-330, 1995 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f
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A;Cross-references: UNIPROT:Q61307; UNIPARC:UP10000028367; EMBL:L40632; NID:g710548; PID:
A;Experimental source: strain C57BL/6J; kidney
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541 FTALQMG-----NENVQQLLQEGISLGNSEADRQ--LLEAAKAGDVETVKKLCTV-QSVN 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 ACRNGDVER----VKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 RDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQH 220
                                                                                                                                                                           653 VKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDL-VKDGDT
                                                                                                                                                                                                       645 DIATTLLEYGADANAVTROGIASVHLAAQEGHVDMVSLLLGRNANVNLSNKSG--LTPLH
                                                                                                                                                                                                                                                                                                                                                            LAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jul-2004
                                       ETALHMAARSGQAEVVRYLVQDGAQVEAKAKDDQTPLHISARLGKADIVQQLLQQGASPN
                                                                                                                                                                                                                                                                    DIQDLL-------RGDAALLDAAKKGCLARVKKLSSPD-NVNCRDTQGRHSTPLH
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                                                                                                                 AATTSG--YTPLHLSAREGHEDVAAFLLDHGASLSITTKKGFTPLHVAAKYGKLEVANLL
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Best Local Similarity 30.6%; Pred. No. 5.7e-46;
Matches 287; Conservative 127; Mismatches 380; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: Z22237; MUID:95340633; PMID:7615634
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ELG 893
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A;Introns: 855/1
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A;Molecule type: mRNA
A;Residues: 1-4377 «KOR»
A;Cross-references: UNIPROT:Q12955; UNIPARC:UP1000013C497; GB:U13616; NID:g608024; PIDN:
                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 AAAVDFTARNDITPLHVASKRGNANMVKLLLDRGAKIDAKTRDGLTPLHCGARSGHEQVV 317
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                                                                                                                                                                                                                                                                                                                                                            membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                           <AN03>
                                                                                                                                                                                                                                                                                                                                                                               73-105/Domain: ankyrin repeat homology <AN01>106-138/Domain: ankyrin repeat homology <AN02>
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                                                                                                                                                                                                                                                                 ;Gene: GDB:ANK3
;Cross-references: GDB:424503; OMIM:600465
                                                                                                                                                                                                                                                                                                                                                                                                   :106-138/Domain: ankyrin repeat homology :139-171/Domain: ankyrin repeat homology 172-200/Domain: ankyrin repeat homology
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C,Superfamily: EGF homology
C,Keywords: alternative splicing;
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A;Molecule type: mRNA
A;Residues: 1-1940 <PET>
A;Cross-references: UNIPROT;Q61307; UNIPARC:UPI0000029ABD; EMBL:L40632; NID:g710548; PID: A;Experimental source: strain C57BL/6J; kidney
C;Genetics:
A;Gene: Ank3
A;Gene: Ank3
A;Introns: 834/1
C;Superfamily: ankyrin; ankyrin repeat homology
C;Superfamily: ankyrin; splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 IVOLLLOHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 RSGHEQVVEMLLDRSA-PILSKTKN-------328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                705 L-VKDGDTDIQDLL------RGDAALLDAAKKGCLARVKKLSSPD-NVNCRDTQ 750
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                                                                                                                                                                                                                                                                                                                     55 ONGLNA--LHLASKEGHVEVVSELLQREANVDAATKKGNTALHIASLAGQAEVVKVLVTN 112
                                                                                                                                                                                                                                                                                                                                                                                                                          243 KAVLTGEYK---KDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 SKNRVEVCSILLSYGADPTILINCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 RIKKHLSLEMVNFKH-----PQTHETALHCAAASPYPKRKQICELLLRKGANINEKTK 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      560 KLEVASLLLOKSASPDAAGKSGLTPLHVAAHYDNQKVALLLLDQGASPHAAAKNGYTPLH
                                                                                                                                                                                                                                                         128 TAGRKSTPLHFAAGFGRKDVVEYLLONGANVQARDDGGLIPLHNACSFGHAEVVNLLLRH
                                                                                                                                                                                                                                                                                                                                                                                   68 AVAAARIMSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRD
                                                                                                                                                                                                                                                                                                                                                                GADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLA----DPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 EFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 CTV-QSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502 LOOGASPNAATTSG--YTPLHLAARECHEDVAAFLLDHGASLSITTKKGFTPLHVAAKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       645 HYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLD
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                                                                                                                                                                       Query Match
13.8%; Score 889; DB 2; Length 1940;
Best Local Similarity 27.9%; Pred. No. 7.5e-46;
Matches 337; Conservative 168; Mismatches 496; Indels 206;
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C;Species: Mus musculus (house mouse)
C;Date: ll-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42715
R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.J., Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.
A;Reference number: Z22237; MUID:95340633; PMID:7615634
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                                                                                                                                                                            VTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAP 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATADALSSGPSSPSSLSAASSLDNLS-GSFSELSSVVSSSGTEGASSLEKKEVPGVDFSI 952
                                                GAEPTIRNTDGRTALDLA----DPSAKAVLTGEYK---KDELLESARSGNEEKMMALLT 272
                                                                                                                                                                                                                                                                      ------GLSPLHMATQGD-----HLNCVQLLLQHNVPVDDVTNDYLTALHVA 357
   393 TPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKH------PQTHETALHCA
                                                                                                                                                                                                                                                                                                      AASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDN
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A;Accession: T42715 A;Status: preliminary; translated from GB/EMBL/DDBJ

811 CVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS-----ADD

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52 ASKEGHVKMVVELLHKE-IILETTTKKGNTALHIAALAGODEVVRELVNYGANVNAQSQK 110
                                                                                                                                                                                                                                                                                105 ACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDG 164
                                                                                                                                                                                                                                                                                                                                                                           338 HLTPLHVAA---HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVMELLLKTG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                            276 VNCHASD------GRKS-----TPLHLAAGYNRVKIVQLLLQHGADVHAKDKG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 DLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 TLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQT 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 DVETVKKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVP 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 ASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815 TDKWAFTPLHEAAQKGRTQLCALLLAHGADFTLKNQEGQTPLDL------VS 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      885 VLNGVRSPGATADALSSGPSSPSSLS----AASSLDNLSGSFSELSSVVSSSGTEGASS 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696 NRDGNTPLDL-VKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHS 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 IAAHYENLANVAQLLIANRGSSVNFTPQNGITPLHIASRRGNVIMVRLLLDRGAQIETKTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 GLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTPLHBAAIKGKIDVCIVLLQHGAEP
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                                                                                                                     Gaps
                                                                                                                  307;
                                                                          Length 1856;
                                                                                                                  Indels
                                                                     Query Match 13.6%; Score 880.5; DB 2; Best Local Similarity 26.0%; Pred. No. 2.3e-45; Matches 294; Conservative 156; Mismatches 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 QLLQE-----GISLGNSEADRQLLE
F;733-765/Domain: ankyrin repeat homology <AN22>F;766-798/Domain: ankyrin repeat homology <AN23>
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R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A;Title: CDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370; PMID:1689849
A;Accession: B35049
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1084 INGMDEELDSPEEL--GTKRICRIITKDFPQ-----YFAVVSRIKQESNQ-1126
                                                                                                                                                                                                                              G-----HRHKLI------KGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDD 1036
                                                                                                                                                                                                                                                           | ::| | : | ::| | ::| | 374 GGSMRGSRHHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPWVEGEGLASRLVEMGPAG 1033
                                                                                                                                                                                                                                                                                                                       1037 KEFQS-VEREMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWE--RYTHRRKEVSE- 1092
                                                                                                                                                                                                                                                                                                                                                                    AOPLGPVIVEIP------HFGSMRGKERELIVLRSENGETWKEHQPDSKNEDLAEL 1083
                                                                                                                                                                                                                                                                                                                                                                                                                  ----ENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENS---SKSNQY 1145
798 LKVVTEEIMTTTTITEKHKANVPETANEVLDMSDDEGDKCTWFKIPKVQEVLVKSEDAIT 857
                                                                                                                                   EKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVL-----VEMGHKELKEIGINAY 994
                                                                                                                                                                            918 EELLVPSKEOHLT-PTREFDSDSLRH-YSWAADTLDNVNLVSSPVHSGF--LVSFMVDAR 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
.Contains ankyrin 2.2, erythrocyte
.Species: Homo sapiens (man)
.bate: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
                                             -----SSPSSLSAASSLDNLSGSFSELSSVVS----SSGTEGASSL
                                                                                      858 GDTDKYLGPQDLKELGDDSLPAEGYVGFSLGARSASLRSFSSDRSYTLNRSSYARDSMMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;44-76/Domain: ankyrin repeat homology cAN01>
F;77-109/Domain: ankyrin repeat homology cAN02>
F;710-142/Domain: ankyrin repeat homology cAN03>
F;143-171/Domain: ankyrin repeat homology cAN04>
F;122-204/Domain: ankyrin repeat homology cAN05>
F;238-270/Domain: ankyrin repeat homology cAN05>
F;231-203/Domain: ankyrin repeat homology cAN06>
F;304-336/Domain: ankyrin repeat homology cAN09>
F;304-336/Domain: ankyrin repeat homology cAN09>
F;337-369/Domain: ankyrin repeat homology cAN09>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GDB:118737; OMIM:182900
Map position: 8p11.2-8p11.2
Superfamily: ankyrin; ankyrin repeat homology
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;Residues: 1-1856 <LAM>
;Cross-references: UNIPARC:UP10000177546
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F;667-699/Domain: ankyrin repeat
F;700-732/Domain: ankyrin repeat
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DD 171 KVRLPALHIAARNDDTRIAAVLLQNDPNPDVLSKTGFTPLH 211 QY 276 VNCHASDGRKSPPLHLAAGYNRVKIVQLLLQHGADVHAKDKG 317 DD 212 IAAHYENLAVAQLLLANGSSVNFTPQNGITPLHIASRGNVIMVRLLLDRGAGTEKTKD 271 QY 318 DLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHBAASKNRVEVCSLLLSYGADD 377 DD 272 ELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHWAAQGBHLDCVRLLLQYDAE- 330	378 TLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQT	0	STATEMENT	Qy 1000 LIKGVERLISGQGINPYLTINTSGSGTILIDLSP 1034
Db 902 ISPVASPVHTGFLVSFM	RESULT 7 A35049 ankyrin 1, erythrocyte splice form 2 - human N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R N;Alternate names: ankyrin 2.2, erythrocyte C;Species: Homo sapiens (man) C;Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004 C;Accession: A35049 R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990 A;Reference for human erythrocyte ankyrin. A;Reference for human erythrocyte ankyrin. A;Reference A35049; MUID:90175370; PMID:1689849 A;Accession: A35049 A;Reteria: preliminary A;Reaidues: 1-1880 <lam></lam>	A;Cross-references: UNIPROT:P16157; UNIPARC:UP10000177545; GB:M28880 A;Genetics: A;Genetics: A;Genetics: A;Genetics: C;Genetics: B;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: B;Genetics: F;238-270/Domain: ankyrin repeat homology <an07> F;238-270/Domain: ankyrin repeat homology <an08> F;237-369/Domain: ankyrin repeat homology <an09> F;337-369/Domain: ankyrin repeat homology <an10> F;337-369/Domain: ankyrin repeat homology <an11> F;403-435/Domain: ankyrin repeat homology <an12> F;469-501/Domain: ankyrin repeat homology <an13> F;469-501/Domain: ankyrin repeat homology <an15> F;564-667/Domain: ankyrin repeat homology <an15> F;568-600/Domain: ankyrin repeat homology <an15> F;668-600/Domain: ankyrin repeat homology <an19> F;661-633/Domain: ankyrin repeat homology <an19> F;671-695/Domain: ankyrin repeat homology <an12> F;671-695/Domain: ankyrin repeat homology <an20> F;700-732/Domain: ankyrin repeat homo</an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an20></an12></an19></an19></an19></an19></an19></an15></an15></an15></an13></an12></an11></an10></an09></an08></an07>	Query Match Query Match Query Match Query Match Query Match 13.6	

Matches 295 QY 105 DD 111 QY 225 DD 171 QY 276 DD 272 QY 318 DD 331 QY 438 DD 331 QY 438 DD 335 QY 455 QY 637	Db S73 IHVAVHHNILDIVKLILPRGGSPH-SPAWRGYTPLHIAAKQNQVEVARSLLQYGGSANAE 631 Op G96 NPGNTPLDL-VKCGPTDIQDLRGDAALLDAAKKGCLARVKKLSSPDNYNCRDTGCRHS 754 Db G32 SVGCVTPLHLAAGEGHAEMVALL
C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004 C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004 Spilous: 30-Sep-1991 #sequence revision with the companient of the com	F;2-837/Region: anion exchange protein binding F;2-837/Region: anion exchange protein binding F;2-109/Domain: ankyrin repeat homology <an01> F;17-109/Domain: ankyrin repeat homology <an03> F;110-124/Domain: ankyrin repeat homology <an05> F;110-204/Domain: ankyrin repeat homology <an06> F;112-204/Domain: ankyrin repeat homology <an06> F;238-270/Domain: ankyrin repeat homology <an06> F;238-270/Domain: ankyrin repeat homology <an06> F;238-270/Domain: ankyrin repeat homology <an09> F;337-369/Domain: ankyrin repeat homology <an10> F;304-336/Domain: ankyrin repeat homology <an11> F;403-436/Domain: ankyrin repeat homology <an11> F;403-435/Domain: ankyrin repeat homology <an14> F;502-534/Domain: ankyrin repeat homology <an15> F;502-534/Domain: ankyrin repeat homology <an16> F;601-633/Domain: ankyrin repeat homology <an18> F;601-633/Domain: ankyrin repeat homology <an18> F;601-633/Domain: ankyrin repeat homology <an18> F;601-633/Domain: ankyrin repeat homology <an18> F;601-633/Domain: ankyrin repeat homology <an18> F;601-633/Domain: ankyrin repeat homology <an12> F;601-633/Domain: ankyrin repeat homology <an12> F;601-633/Domain: ankyrin repeat homology <an12> F;601-633/Domain: ankyrin repeat homology <an12> F;601-633/Domain: ankyrin repeat homology <an12> F;601-633/Domain: ankyrin repeat homology <an18> F;601-633/Domain: 62K #status predicted <dom2> F;828-1382/Region: spectrin binding F;133-1881/Domain: 55K #status predicted <dom3> F;828-1382/Region: spectrin binding F;864 Focal Similarity 25:8 F; Fred. No. 3.2e-45;</dom3></dom2></an18></an12></an12></an12></an12></an12></an18></an18></an18></an18></an18></an16></an15></an14></an11></an11></an10></an09></an06></an06></an06></an06></an05></an03></an01>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 ACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHN 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 ACRNGDVER-VKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 AARAGNLDKVVEYLKGGIDINTCNQNGLNA--LHLAAKEGHVGLVQELLGRGSSVDSATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 PTIRNTDGRT----ALDLADPSAKAVLTGEYKKDEL----LESARSGNEEKWMALLTPLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 KSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHP-----QTHE
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                    Length 3924;
                                                                                                                                                                                                                                                                                                                                                          Score 877; DB 2;
Pred. No. 1.2e-44;
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F;760-792/Domain: ankyrin repeat homology
F;793-825/Domain: ankyrin repeat homology
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                        F;496-528/Domain: ankyrin repeat hor F;529-561/Domain: ankyrin repeat hor F;525-594/Domain: ankyrin repeat hor F;555-627/Domain: ankyrin repeat hor F;628-660/Domain: ankyrin repeat hor F;64-726/Domain: ankyrin repeat hor F;727-759/Domain: ankyrin repeat hor F;727-759/Domain: ankyrin repeat hor F;760-792/Domain:                                                                                                                                                                                                                                                                                                                                                      13.6%;
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A;Residues: 1-3924 <CHA>
A;Cross-references: UNIPROT:Q01484; UNIPARC:UPI0000125B19; EMBL:Z26634; NID:g406287; PIC
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A, Residues: 463-474, PB', 477-495 <TSE>
A, Cross-references: UNIPARC:UPID:000016A55B; GB:M37123; NID:g178647; PIDN:AAA6282B.1; PID:
R, Chan, W.; Kordeli, B.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A, Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and se
A, Reference number: A49462; MUID:94075409; PMID:8253844
                                                                                                                                                                                                                                  ankyrin 2, neuronal long splice form - human
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N;Contains: ankyrin 2, short form
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
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2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
                                 -----DDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCN 1076
                                                                                     993 IPHFASHGRGDRELVVLRSENGSVWKEHR-----SRYGESYLDQILN 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiOtto, E.; Kunimotto, M.; McLaughlin, T.; Bennett, V. Call Biol. 114, 241-253, 1991
A; Title: Isolation and characterization of CDNAs encoding A; Reference number: A39643; MUID:91302466; PMID:1830053
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A;Molecule type: mRNA
A;Residues: 1-2077 <OT1>
A;Cross-references: UNIFARC:UPI0000177547; GB:X56957
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submitted to the EMBL Data Library, September 1993
A; Reference number: S37431
A; Accession: S37431
A; Status: preliminary
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homology <AN112+
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A;Map position: 4q25-4q27
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F;162-190/Domain: ankyrin repeat
F;191-223/Domain: ankyrin repeat
F;232-264/Domain: ankyrin repeat
F;265-297/Domain: ankyrin repeat
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A; Residues: 1-3924 < RES>
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;Accession: 149502
;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
amm. Genome 3, 281-285, 1992
;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory dome;
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Cross-references: UNIPROT:Q02357; UNIPARC:UPI000002921E; GB:M84756; NID:g191939; PIDN:
318 DLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADP 377
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Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                         438 HETALHCAAASPYPKRKOICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHE
                                                                                                                                                                                   498 AKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQM----GNENVQQ
                                                                                                                                                                                                                                                                   LHNACSYGHYEVAELLVKHGAVVNVADLWK-FTPLHEAAAKGKYEICKLLLQHGADPTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 NRDGNTPLDL-VKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       815 TDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL-----VSADDVSALL
                                                                              378 TLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQT
                                                                                                                                                                                                                                                                                                                                                              459 YLLONKAKANAKAKDDOTPLHCAARIGHTGMVKLLLENGASPNLATTAGHTPLHTAAREG
                                                                                                                                                                                                                                                                                                                                                                                                        578 DVETVKKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVP
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Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
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<AN07>
<AN08>
<AN09>
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139-167/Domain: ankyrin repeat homology <AN04>
1201-233/Domain: ankyrin repeat homology <AN06>
1201-233/Domain: ankyrin repeat homology <AN06>
1234-266/Domain: ankyrin repeat homology <AN07>
1330-3299/Domain: ankyrin repeat homology <AN07>
1300-332/Domain: ankyrin repeat homology <AN09>
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Keywords: alternative splicing
40-72/Domain: ankyrin repeat homology <AN01>
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Wolecule type: mRNA
Residues: 1-1848 *BIR>
Cross-references: UNIPROT:Q61302; UNIPARC:UPI0000028360; EMBL:X69063; NID:g311816; PIC
Superfemily: ankyrin; ankyrin repeat homology
Keywords: alternative splicing
*8e/pomain: ankyrin repeat homology <AN01>
                                                                                                                                                                                                                                                                                                                                             Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E. . Biol. Chem. 268, 9533-9540, 1993
, Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found flaeference number: S37771; MUID:93252825; PMID:8486643
                                                                                      ELGDDSLPSSQFLDGMNYLRYSLEGGRSDSLRSFSSDRSHTLSHAS--YLRDSAVMDDSV 926
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                                                                                                                                                                                                                                                                                                                            Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                                                           926 ----SSVVSSSGTEGASSLEKKEVPGVDFSITQFV--RNLGLEHLMDIFEREQITLDVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 ACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHPAAGFGRKDVVEYLLQNGANVQARDDG
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larity 29.7%; Pred. No. 4.4e-45;
Conservative 132; Mismatches 281; Indels 178;
                                                                                                                                           EMGHKELKEIGINAYGHRHKLIKGVERL 1007
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPB
PTRRSVEPEBHRHSQHEDHEGST' <GA4>
A, CTOSS-references: UNIPARC: UP100007D1A6; EMBL: U50071; NID: G1208871; PID: G1208876; PIDN
A, CTOSS-references: UNIPARC: UP100007D1A6; EMBL: U50071; NID: G1208871; PID: G1208876; PIDN
A, CG-11 Biol. 129, 1081-1092, 1995
A,Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae
A, Reference number: A57282; MUID: 95263663; PMID: 7744957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-1000, 'SKLQHRT',1002-1718,'KWEELNRL',1727,'D','ES',1942,'PSPAGRS',1950,'IVA
32,'S',2034-2035,'GSPTRRSVEPEEHHSQHEDHEGST' <GA2>
A;Cross-references: UNIPARC:UPI0000077BDB; EMBL:U50071; NID:g1208871; PID:g1208875; PIDN
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A;Molecule type: DNA
A;Residues: 1-1718, 'KW',1903-1905,'NRLADESSPS',1916-1917,'QRSTIVAESTSEQVPE',1934-1935,'E
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A;Molecule type: DNA
A;Residues: 1-2039 <GAT>
A;Ccose-references: UNIPROT:Q17489; UNIPARC:UPI0000077865; EMBL:U50071; NID:g1208871;
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text change 09-Jul-2004
C;Accession: T15347; T15346; T15345; A57282; B57282; C57282
R;Gattung, S.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid B0350.
A;Reference number: Z18332
                                                                                                             SERTENGYTPLHMAAHYGHLDLVKFFIENDADIEMSSNIGYTPLHQAAQQGHIMINLLL
DAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADV
                           AHGADPTLKNOEGOTPLDLVSADDVSALLTAAMPPSALPSCYKPOVLNG-----V
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                                                                                    NAQDKGGLI PLHNAAS YGHVDVAALLI KYNACVNATDKWAFTPLHEAAQKGRTQLCALLL
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                                                                                                                                                                                                                                                            RSPGATADALSSGPSSPSSLSAAS-----SLDNLSGSFSELSSVVSSSGTE----GAS
                                                                                                                                                                                                                                                                                       -----SRVRQEVHVIGPDGGT 1092
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                                        684 YGVISAAAKNGL------
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A;Status: preliminary
A;Molecule type: DNA
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 194, 'f', 196, 'I',198, 'DC',201,'G',409,'AV',412,'Q',414,824,'S',826,'ER',829,'E
A;Residues: 194,'E', 193,'QV',1836,'E',1934-1935,'EQS',1939,'ESES',1944,'REDDGTIVTT',194£
A;CTOSB-references: UNIPARC:UPI0000076E32; GB:U21732; NID:9790603; PIDN:AAA85853.1; PID:§
A;Residues: 1-852,'GGG',856-1000,'SKLQHRT',1002-1319,'IG',1322-1595,'DA',1598-1718,'KWEEI','SHRED',2007-2008,'TI',2011,2017,'TT',2020-2022,'SHIS' <OTS>
A;Cross-references: UNIPARC:UPI0000080E35; GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:çA;Accession: B57282
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A;Residues: 831-852,'GGG',856-1319,'IG',1322-1595,'DA',1598-1718,'KWEELNRL',1727,1799,'E'
V',1945-1947,'VT',1950,'SH',1975,'SESP',1980-1981,'SPTRRSVEPEEHRHS',1984-1985,'EDHEGS',11
A;Cross-references: UNIPARC:UPI000017754A, GB:U21731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ajintrons: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979, C; Superfamily: ankyrin; ankyrin repeat homology cander for ankyrin repeat homology cander for ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat homology cander fisse-390/Domain: ankyrin repeat fisse-390/Domain fisse-390/Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 858; DB 2; 26.3%; Pred. No. 6.5e-44;
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319; Conserv
                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: C57282
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1A9; GB:AE001254; GB:AE000520; NID:
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idambaram, M.; Utterback, T.; McDor
                                                n, the syphilis spirochete.
                                                                                                      OLAPTPQLKER---LAYEFK 405
                                                                                                                                                                                                                NALDNLGQTSLHRAAYCGH 519
:: | |:|:| ||:|
DIRDEKGRTALDLAAFKGH 427
                                                                                                                                                                                                                                                                    SIGNSEADRQLIEAAKAGDV 579
|:: | | | | |
INGHTLCLRILLEIAD--- 473
                                                                                                                                                                                                                                                                                                                          QHGADVHAKDKGGLVPLHN 639
                                                                                                                                                                                                                                                                                                                                                                               SICKLLLOHG---ADPTKKN 696
                                                                                                                                                                                                                                                                                                                                                                                                                                     AALLDAAKKGÇLARVKKLS 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | : | SALINDHG--NCASLLLGAI 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAODKGGLIPLHNAASYGHV 799
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-----STP----L 289
                      WLSAGFEIDTPDKFGRTCL 224
                                                                                                                                                           HCAAASPYPKRKQICELLL 461
                                                                                                                                                                            :| ||| : :| ||||
|HYAAAYGH---RQCLELLL 367
                                                                                                                                                                                                                                                                                                                                              WLSELLOMALSEEDCCFKD 584
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xt_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 934;
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Best Local Matches 25	cal S 254	Similarity 23.8%; Pred. No. 2.2e-26; 254; Conservative 159; Mismatches 373; Indels 281; Gaps	36;
Ż:	98	ACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRK	145
ą	24	: : :: : :	78
٠ ج		DVVEYILQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLEHGADPNARDNWNYTPLH	203
Ω		DAHVVDFLLSMGADTEAQDASGSTFLMVAVTENCFESVRMLIARDASLFSRDAQGDTFLT	138
≿ a	204	EAAIKGKIDVCIVGAEPTIRNTDGRTA	234 198
≿	235	LDLADPSAKAVLTGEYKKDELLESARSGNEEKMALLTPLAVNCHASDGRKSTPLHLA 	292
ą	199	LSLAYSSSSDARAAEVAADLLLGGAELMHGSFSBFEIAVLKRNYDLHFTDGSTPLHVM	256
Σ ብ	293	AGYNRVKI VOLLIQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLMQF	352
≿ :	353	TPLHEAASKNRVEVCSLLLSYGADPTLINCHNKSAIDL-APTPOLKERLAYEFKGHSLLO	411
ą	284	TPLHEAVRAGQVDAAVLLLRSGADPNVRDASGNTCLHLVAPAP-FRVRLVGALLD	337
≱	412	RIKKHLSLEMVNF	471
ភ	338	AGASVAIKDDYGETPLHVAARLGMDRAFVERLVGAGADISERN	380
<u>≻</u> .		KEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGGTSLHRAAYCGHLQTCRLLLS	528
ū	381	KKGETPLVLTIDRDHRDLTAYFVSLGADIHAEDMRGETPLTKALARG-LETVKIVVTDSN	439
۶		NVQQLLQEGISLGNSEA : :	582
Д	440	LYKQDVVGRDPLHVAVSRRAHLDIVKFLFREPKQMI	475
γ	583	KKLCTVQSVNCRDIBGRQSTPLHFAAGYNRVSVVBYLLQHGAD	625
Д	476	AVANDDRAVGE	523
>	626		671
Д	524	DTGGNTPLHLACE	583
>	672	EAAAKGKYEICKLILQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGC	731
ą	584	SAVKSDAAEVISILLHPQAGNPALVDA	610
~	732	LARVKKLSSPDNVNCRDTQCRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGG	786
ą	611	RDAVGNTVLHACVRWSALRSADVLIREADARHVSLLNARNLSG	653
£.	787	LIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADFT	846
ð	654	KPPLHLAARAGNVDFIRLLLSHRVALHMGDETGKSALTDAVLADQEESVHMLLSAGANPV	713
¥:	847	LKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSP	906
ą	714	QODMYGRTPLHEAVLCNSQSVIAALRAAGNPFARDSYGTTP	755
≿	907	SSLSAASSLDNLSGSPSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEH	963
ą	756	LSLALLKG-DTFVGAVVGKDPLIANSDGQTPLHLAVMENVPVQTFRLLLAK	805
ž	964	LMDIPEREQITLDVIVEMGHKELKEIGINAYGHRHKLIK-GVERLISGQQGLNPYLT	1019
ą	908	-	828
ž:	1020	LNTSGSGTIL-IDLSPDDKEFQSVEEEMQSTVREHRDG 1056	

859 KNTSILKTLVGFAVNKTDSAGESILHYAAKVADEKTLQGLLAMNRFG 905

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Search completed: December 18, 2006, 17:35:54 Job time : 46.1952 secs

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

December 18, 2006, 17:21:50 ; Search time 248 Seconds (without alignments) 4625.078 Million cell updates/sec Run on:

US-10-616-101-4 6464 1 RCSARRGAAGGQGAQRGARV.....AYPEYLITYQIMRPEGMVDG 1240 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2849598 seqs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Q9h2k2 homo sapien	gallu		mus n		gallu			Q59fx0 homo sapien						_	Q3ues3 m adult mal	Q6p537 mus musculu	Q4fzm0 xenopus lae		Q574d7 rattus norv	bog t	homo	mus n	Q4u256 mus musculu	homo	mus n	Q12955 homo sapien	พน8 ส	Q4u257 mus musculu	O88521 rattus norv	070511 rattus norv
	TNKS2 HUMAN	Q800EO CHICK	TNKS1 HUMAN	Q6PFX9 MOUSE	Q4G0F2_HUMAN	Q800D9_CHICK	OSXGKS_XENLA	Q4RG97_TETNG	QS9FX0_HUMAN	Q8BX62_MOUSE	Q7PYH8_ANOGA	Q9VBP3_DROME	Q9XZ37_DROME	Q4S372_TETNG	Q8BXH7_MOUSE	Q3UES3_MOUSE	Q6P537 MOUSE	Q4FZM0_XENLA	Q574D8_RAT	Q574D7_RAT	Q9N180_BOVIN	Q7Z3G4_HUMAN	Q4U258_MOUSE	Q4U256_MOUSE	Q5CZH9_HUMAN	QBVC68_MOUSE	ANK3 HUMAN	Q4U259 MOUSE	Q4U257 MOUSE		070511_RAT
80	-	~	1	7	7									~											7	7	Н	7	N	0	7
Length	1166	1167	1327	1320	1327	1266	1303	1212	1055	916	1168	1181		-					_	1984	1136	1861	1765	1961	1861	1726	4377	1943	1940	1762	2622
	94.5	σ	79.0	78.9	78.8	78.5	77.5	75.4	72.4	66.3	64.3	62.0	61.8	51.4	47.4	46.6	31.9	30.1	14.0	14.0	14.0	13.9	•	٠	13.8		٠	•	13.8	•	13.7
Scor	6108	5760.5	5103.5	5098	5095.5	5074	5010.5	4875.5	4681.5	4285.5	4156.5	4005	3997	3324	3066	3013	2063	1944.5	906	906	904	897	895	895	894	893	•	891	æ	888.5	885.5
Result No.	-	7	٣	4	ហ	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56		28			31

Q5vxd5 homo sapien	Q99407 homo sapien	Q13768 homo sapien	P16157 homo sapien	O59fp2 homo sapien	Q01484 homo sapien	Q61302 mus musculu	Q3uh42 mus musculu	Q3uhp2 mus musculu	Q4rt14 tetraodon n	Q4rnf0 tetraodon n	Q02357 mus musculu	mus
QSVXDS_HUMAN	099407 HUMAN	Q13768 HUMAN	ANK1 HUMAN	Q59FP2 HUMAN	ANK2 HUMAN	Q61302 MOUSE	Q3UH42 MOUSE	Q3UHP2 MOUSE	Q4RT14 TETNG	Q4RNF0 TETNG	ANK1 MOUSE	Q8C8R3_MOUSE
010	10	7	Н	7	н	~	7	7	7	~	~	7
4372	1856	1719	1880	1899	3924	1848	1878	1907	1950	4408	1862	1219
13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.5	13.5	13.5
882	880	878.5	878.5	877	877	876	876	876	876	875.5	874	872
32	η 4	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 TUNKS2 HUMAN 1 AD TUNKS2 HUMAN 1 DT 27-MAR DT 07-MAR DT 07-MAR DT 07-MAR DE INCERING 9 COC HOMO.

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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License CATALTIC ACTIVITY: NDD(+) + (ADP-D-ribosyl) (n)-acceptor = nicotinamide + (ADP-D-ribosyl) (n+1)-acceptor.

BUBNIT: Oligomerizes and associates with TNKS. Interacts with the cytoplasmic domain of ATMSP/Otase in SLC2A4/GiuT4-vesicles. Binds to the N-terminus of Grb14 and TRF1 with its ankyrin repeat TISSUE SPECIFICITY: Highly expressed in placenta, skeletal muscle, liver, brain, kidney, heart, thymus, spinal cord, lung, peripheral blood leukocytes, pancreas, lymph nodes, spleen, prostate, testis, ovary, small intestine, colon, mammary gland, breast and breast carcinoma, and in common-type meningloma. Highly expressed in fetal liver, heart and brain.

FYM: ADP-ribosylated (-auto).

SIMILARITY: Contains 15 ANK repeats.

SIMILARITY: Contains 15 ANK retaile alpha motif) domain. Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002; Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.; "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2 SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC284/GUT4-vesicles. Also Gound around the pericentriolar matrix of mitoric centromeres. During interphase, small fraction of TNKS2 is found in the nucleus, associated with Annual telomores.";
Mol. Cell. Biol. 22:332-342(2002).
-!- FUNCTION! May regulate vesicle trafficking and modulate the subcellular distribution of SLC344(GLUT4-vesicles. Has PARP activity and can modify TRF1, and thereby contribute to the regulation of telomere length. Glycosyltransferase; Golgi stack; NAD; Nuclear protein; Repeat; PROSITE; PS50297; ANK REP_REGION; 1.
PROSITE; PS50088; ANK REPEAT; 15.
PROSITE; PS51059; PARP_CATALYTIC; 1.
PROSITE; PS50105; SAM DOMAIN; 1.
ADP-ribosylation; ANK repeat; Chromosomal protein; Tankyrase 2. /FTId=PRO_0000211334. ANK 1. ANK 2. EMBL, AF305081, AAG25674.1, ALT INIT, MRNA.
EMBL, AF205081, AAG44694.1, MRNA.
EMBL, AF32696, AAK13463.1, -; MRNA.
EMBL, AF309031, AAK35811.1; -; MRNA.
EMBL, AF309033, AAK52581.1; -; MRNA.
EMBL, AF300033, AAK62330.1; -; MRNA.
EMBL, AF31007, CAC78760.1; -; Genomic_DNA.
EMBL, AK023746; BAB14665.1; ALT_INIT; MRNA. HSSP; P16157; 1N11. Ensembl; ENSG00000107854; Homo sapiens. MIM; 607128; gene.
InterPro; IPR001290; PARP.
InterPro; IPR0112317; PARP catalytic.
InterPro; IPR01160; SAM.
InterPro; IPR011510; SAM.
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InterPro; IPR011510; SAM.
InterPro; IPR011510; SAM.
InterPro; IPR FUNCTION, AND ADP-RIBOSYLATION Nat. Genet. 36:40-45(2004). HGNC; HGNC:15677; TNKS2. Celomere; Transferase region REPEAT

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SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TERF1.
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                  MEDLINE=99040105; PubMed=9822378; DOI=10.1126/science.282.5393.1484;
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION.
MEDLINE=99454782; PubMed=10523501;
SMith S., de Lange T.,
"Cell cycle dependent localization of the telomeric PARP, tankyrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
BABDINES-21602891, Pubmed=11739745; DOI=10.1128/MCB.22.1.332-342.200
COOK B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION, AND PHOSPHORYLATION.
MEDLINE=20556282; PubMed=10988299; DOI=10.1074/jbc.M007635200;
Chi N.-W., Lodiah H.F.;
"Tankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                Smith S., Giriat I., Schmitt A., de Lange T.;
"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487 (1998).
              TNK51 HUMAN STANDARD; PRT; 1327 AA.

095271; 095272;
27-MAR-2002, integrated into UniProtKB/Swiss-Prot.

01-MAY-1999, sequence version 1.

07-MAR-2006, entry version 45.

Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) (TRF1-interacting ankyrin-related ADP-ribose polymerase).

Name=TNKS; Synonyms=PARPSA, PARPL, TINI, TINF1, TNKS1;

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION IN A COMPLEX WITH POT1; TERF1 AND TINF2.
MEDLINE=22711258; PubMed=12768206; DOI=10.1038/nature01688;
Loayza D., De Lange T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=095271-2; Sequence=VSP_004538, VSP_004
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                     to nuclear pore complexes and centrosomes."; J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 22:332-342(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human telomeres.";
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                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                   /FTId=VSP 004538.
Missing (In isoform 2).
/FTId=VSP 004539.
H->A: Loss of activity; when associated
TISSUE SPECIFICITY: Ubiquitous; highest levels in testis. PTM: Phosphorylated on serine residues by MAPK kinases upon insulin stimulation.

PTM: ADP-Tibosylated (-auto).

SIMILARITY: Contains 15 ANK repeats.

SIMILARITY: Contains 15 ANK repeats.

SIMILARITY: Contains 1 PARP catalytic domain.

SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.
                                                                                                                                                                                                                                                                                                                                                           Length 1327;
                                                                                                                                                                                                                                                                                                                                        >A: Loss of activity; when
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Poly-His.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV
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                                         AAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLALLLAVAAARIMSGRRCA
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               Indels
            963; Conservative 110; Mismatches 128;
79.2%; Pred. No. 1.7e-291;
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Indels
                                                                                                                                                                                    1320 AA; 140944 MW; A90360DC665FFCC0
                                                                                                                                                                                                                'Match 78.9%; Score 5098; DB 2; Local Similarity 79.2%; Pred. No. 3.6e-291; les 966; Conservative 105; Mismatches 130;
InterPro; IPR011510; SAM_2.
PÉBAN, PP000023, Ank; 19.
PÉAM, PP00044; PARP; 1.
PÉAM, PP0044; SAM_2; 1.
PEALNTS; PR01415; ANKTRIN.
SMART; SM00248; ANK; 15.
SMART; SM00248; ANK; 15.
PROSITE; PS50029; ANK REP REGION; 1.
PROSITE; PS50089; ANK_REPEAT; 15.
PROSITE; PS51059; PARP CATALYTIC; 1.
PROSITE; PS51059; PARP CATALYTIC; 1.
                                                                                                                                                                     ANK repeat; Repeat.
SEQUENCE 1320 AA;
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STRAIN-CSTOBL/6:

TISSUE-Brain;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;

Altschul S.F.; Zeeberg B.B.; Bardow K.H., Schaefer C.F.; Bhat N.K.,

Altschul S.F.; Zeeberg B.B.; Buetow K.H., Schaefer C.F.; Bhat N.K.,

Hopkins R.F.; Jordan H., Moore T., Max S.I.; Wang J., Haich F.,

D. Stapleton M., Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

Brownstein M.J.; Usdin T.B.; Toshiyuki S., Carninci P., Prange C.;

A. Raha S.S., Loquellano N.A.; Peters G.J., Abramson R.D.; Mullahy S.J.,

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Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                1119 QSVEEEMQSTIREHRDGGNAGGIFNRYNVIRIQKVVNKKLRERFCHRQKEVSEENHNHHN 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                               ERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVGIGGGTGCPVHK
                                                                                             DRSCYICHROLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGE
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; BNSMUSGROOO0031529; Mus musculus.
MGI; MGI:1341087; Thks.
GO; GO:000534; C:nucleus; IEA.
GO; GO:0005350; F:NAD+ ADP-ribosyltransferase activity; IEA.
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
InterPro; IPR001210; ANK.
InterPro; IPR012137; PARP.
InterPro; IPR01217; PARP.
InterPro; IPR0160150; SAM.
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Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                           QGPEX9 MOUSE PRELIMINARY; PRT; 1320 AA. QGPEX9; 05-70L-2004, integrated into UniProtKB/TrEMBL 05-70L-2004, sequence version 1. The protein. The protein. Name=Thk9;
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HSSP; Q00420; 1AWC.
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                                                                22 AAHGTAPDPVTAGSQAAR--ALSASSP-GGLALLLAGPGLLLRLLALLLAVAAARIMSGR 78
                                                                                                                                                                                                                                                                                      396 LVPLHNACSYGHYEVTELLLKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 LVNCHGKSAVDMAPTPELRERLTYEFKGHSLLQAAREADLAKVKKTLALEIINFKQPQSH
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                                                                                                                                                       199 YTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799 VDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL
                                                                                                                                    79 RCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679 YEICKLILGHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKL
                                 Gaps
                                  18;
Length 1320;
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CKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSP 741
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 SAAGVAPUPAGSGSNNSPSSSSSPTSSSSSPSSPG----SSLAESPEAAGVSSTAPL
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                                                                        R GO; GO:000564; Citucleus; IEA.

R GO; GO:000564; Citucleus; IEA.

GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR02110; ANK.

InterPro; IPR01217; PARP_catalytic.

R InterPro; IPR01217; PARP_catalytic.

R Pfam; PF00044; PARP; 1.

R Pfam; PF00044; PARP; 1.

R PRINT; PR0044; PARP; 1.

R RAINT; SM0044; SAM 2; 1.

R RNSAT; SM0044; SAM; 1.

R PROSITE; PS50297; ANK REP REGION; 1.

R PROSITE; PS50089; ANK REPEAT; 15.

R PROSITE; PS51059; ANK REPEAT; 15.

R PROSITE; PS51059; ANK RAPP_CATALYTIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.8%; Score 5095.5; DB 2; Best Local Similarity 79.1%; Pred. No. 5.1e-291; Matches 962; Conservative 110; Mismatches 129;
                                                            EMBL; BC098394; AAH98394.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                      ANK repeat; Repeat.
SEQUENCE 1327 AA;
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Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bart N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Haich F.,

A papeleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Tooshlyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Whiting M., Madan A., Young A.M., Sodergren E.J., Lu X., Gibbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallus D.E.,

Boneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                        HENERMLFHGSPFINAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCP 1228
                859 VSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNL
                                             936 ATADDIRALLIDAMPPEALPTCFKPOAT-----WYSASLISPASTPSCLSAASSIDNL
                                                                                               VHKDRSCY1 CHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSVNGLALAEYV1 Y
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                               SGSFSELSSVVSSSGTEGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDIFEREQITLD
                                                                                                                                                                                                           KEFQSVEEEMQSTVREHRDGGHAGGI FNRYNILKIQKVCNKKLWERYTHRRKEVSBENHN
                                                                                                                                                                                                                                                                           HANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OGGOP2-HUMAN PRELIMINARY; PRT; 1327 AA.
04G0P2;
30-AUG-2005, integrated into UniProtKB/TrEMBL.
30-AUG-2006, sequence version 1.
07-PEB-2006, entry version 4.
Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase.
Name=TNKS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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NIH MGC Project;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
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715 DLLKGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQ 774
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InterPro; IPR001660; SAM.
InterPro; IPR011510; SAM_2.
Pfam; PF00023; Ank; 19.
Pfam; PF00044; PARP; 1.
Pfam; PF00644; PARP; 1.
PRINTS; PR01415; ANKTRIN.
SWART; SW00448; ANK; 15.
SWART; SW00454; SAM; 1.
PROSITE; PS50089; ANK REP_REGION; 1.
PROSITE; PS50089; ANK REP_REGION; 1.
PROSITE; PS51059; PARP_CATALYTIC; 1.
PROSITE; PS51059; PARP_CATALYTIC; 1.
PROSITE; PS61016; SAM_DOMAIN; 1.
ANK REPEAT; REPORT.
SEQUENCE 1266 AA; 136212 MW; 14B661
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                                                                                                                                                    AALLIKYNTCVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTMKNQEGQTPLDLATA
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|DIRALLIDAMPPRALPTCFKPQAT-----VVSASLISPASTPSCLSAASSIDNLTGP
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080009;

01-JUN-2003, integrated into UniProtKB/TrEMBL.

01-JUN-2003, sequence version 1.

01-JUN-2006, entry version 14.

Tankyrase 1.

Gallus gallus (Chicken).

Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria, Aves; Neognathae; Galliformes; Phasianinae;

Gallus.
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MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;
DE Rycker M., Venkatesan R.N., Wei C., Price C.M.;
"Vertebrate tankyzese domain structure and sterile alpha motif mediated multimerization.";
Biochem. J. 372:87-96(2003).
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
GO; GO:000471; P:protein amino acid ADP-ribosylation; IEA.
InterPro; IPR001210; ANK.
InterPro; IPR012317; PARP_catalytic.
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HSSP; P16157; 1N11.
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**A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

**A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

**A Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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**A Preby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 'Genetic and genomic tools for Xenopus research: The NIH Xenopus
 PPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPE 1235
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 Dev. Dyn. 225:384-391 (2002)
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Distributed under the Creative Commons Attribution-NoDerivs License
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."!

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 128 TAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRH
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R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005641; P:protein amino acid ADP-ribosylation; IEA.

R GO; GO:0006411; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPRO110; ANK.

R InterPro; IPRO1210; ANK.

R InterPro; IPRO1231; PARP_catalytic.

R InterPro; IPRO11510; SAM.

R InterPro; IPRO11510; SAM.

R Pfam; PF00023; Ank; 18.

R Pfam; PF00044; PARP; 1.

R Pfam; PF0044; PARP; 1.

R PRINT; SN0044; PARP; 1.

R SMART; SN00445; SAM; 15.

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 Klein S., Gerhard D.S.;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
 PROSITE, PS50297; ANK REP REGION; 1. PROSITE; PS50089; ANK REPEAT; 15. PROSITE; PS51059; PARP CATALYTIC; 1. PROSITE; PS50105; SAM_DOMAIN; 1.
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10 Q4RG97_TETNG PRELIMINARY; PRT; 1212 AA.

11 9-JUL-2005, integrated into UniProtKB/TrEMBL.

11 9-JUL-2005, sequence version 1.

12 9-JUL-2006, enery version 5.

13 Chromosome 12 SCAF15104, whole genome shotgun sequence. (Fragment).

14 ORFNames-eSTRENG00034904001;

15 Tetracdon ingroviridis (Green puffer).

16 Tetracdon ingroviridis (Green puffer).

17 C Actinopterygil, Neoplerygil; Teleostel; Buteleostomi;

18 C Actinopterygil; Acanthopterygil; Teleostel; Buteleostel; Neoteleostel;

20 Actinomorpha; Acanthopterygil; Teleostel; Buteleostel;

21 C Tetradontoidea; Tetracdontidae; Tetracdon.

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PubMed=15496914; DOI=10.1038/nature03025;
Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
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Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.
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 82 GGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAG 141
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Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Blemont C., Salli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff J.-N., Gilgo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
 49 IGEKTWMNTFLQTGANVHARDDGGLIPLHNACSFGHAEVVSLLLCHGADPNARDNWNYTP
 109 LHEAAIKGKIDVCIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARS
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 7 GSGAASPIDGSSSIGGAFRELFEACRNGDVSRVKRLV--DSVNV--------
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 Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBE-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.

GO; GO:000641; P:protein amino acid ADP-ribosylation; IEA.

R InterPro; IPR012117; PARP catalytic.

R InterPro; IPR012117; PARP catalytic.

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R Pfam; PF00023; Ank; 15.

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R Pfam; PF00644; PARP; 1.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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QILNENVPTRNSDVDYRFLEAAKAGDLDTVQVSWSLALRLVSEGMRLQKVLSVSQQLCSP
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26-ARR-2005, integrated into UniProtKB/TrEMBL.

26-ARR-2005, sequence version 1.

707-FEB-2006, sequence version 6.

7ankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase variant (Fragment).
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TISSUE-Brain;
TOtocki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
 EMBL, AB209339; BAD92576.1; -; mRNA.

Ensembl; ENSG0000173273; Homo sapiens.

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 STRAIN-C57BL/6J; TISSUB-Cerebellum,
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasaf T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
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TISSUB—Cerebellum; STRAIN=C57BL/6J;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayaehizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
 01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 20.
0 day neonate cerebellum cDNA, RIKEN full-length enriched library,
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ADP-ribose polymerase, full insert sequence.
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A Hill D., Huminlecki L., Iacono M., Tkeck K., Iwama A., Ishikawa T.,
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A Matsuda H., Matsuzawa S., Miki H., Mignone P., Miyake S., Morris K.,
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A Nisson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
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R. Sperling S., Stupka E., Sugiura K., Silva D., Sinclair B.,
R. Amanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
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R. Handura K., Itanamori-Katayama M., Nahon K., Ninomiva N., Nahon K., Imamura K., Itana K., Nord H., Nahon K., Ninomiva N., Ninomiva N., Nahon K., Ninomiva N., Nahon K., Nahon K., Nord N., Nahon K., Nahon K., Nord N., Nahon K., Nahon
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 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 STRAIN=C57BL/63; TISSUE=Cerebellum; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
 STRAIN=C57BL/6J; TISSUB=Cerebellum;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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 Hayashizaki Y.;
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STRANN=C57BL/6J; TISSUB=Cerebellum;
MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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 EMBL; AK048860; BAC33475.1; -; mRNA.
 STRAIN=C57BL/6J; TISSUE=Cerebellum;
 Nature 409:685-690(2001).
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HSSP; P16157; 1N11.

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 ANK repeat, Repeat.
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 Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea; Culicidae;
Anophelinae, Anopheles.
NCBI_TaxID=180454;
 71; Gaps
 The Anophales gambiae Sequence Committee,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003950; F:NMD+ ADP-ribosyltransferase activity; IEA.
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
ANK repeat; Repeat.
SEQUENCE 1168 AA; 126998 MW; 0386A4161210012B CRC64;
 Query Match
Best Local Similarity 65.9%; Pred. No. 9.2e-236;
Matches 791; Conservative 160; Mismatches 178; Indels
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The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 EMBL; AAAB01008987; EAA01120.2; -; Genomic_DNA
 QTPYH8 ANOGA PRELIMINARY; PRT; 1168 AA. Q7PYH8; 15-DEC-2003, integrated into UniProtKB/TrEMBL 06-DEC-2005, sequence version 2. PrEB-2006, entry version 21. ENSANGPO0000018360.
 ORFNames=ENSANGG0000015871;
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 preliminary data.
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STRAIN-PEST;
 NUCLEOTIDE SEQUENCE
 831
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
 Interpro; IPR001290; PARP.
Interpro; IPR012317; PARP_catalytic.
Interpro; IPR011510; SAM_2.
Interpro; IPR011510; SAM_2.
Pfam; PF000024; Ank; 17.
Pfam; PF00644; PARP; 1.
Pfam; PF00644; PARP; 1.
Pfam; PF00644; SAM_2; 1.
SMART; SM00424; SAM_2; 1.
SMART; SM00424; SAM; 15.
 PROSITE; PS50297; ANK REP REGION; 1. PROSITE; PS50089; ANK REPEAT; 14. PROSITE; PS51059; PARP CATALYTIC; 1. PROSITE; PS50105; SAM DOMAIN; I.
 NUCLEOTIDE SEQUENCE.
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 ANK repeat; Repeat.
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 RAMEDLINE-20196006; PubMed-10731132; DOI=10.1126/science.287.5461.2185; RAMEDLINE-20196006; PubMed-10731132; DOI=10.1126/science.287.5461.2185; RAMEDLINE-20196006; PubMed-10731132; DOI=10.1126/science.287.5461.2185; RAMEDLINE-20196006; PubMed-10731132; DOI=10.1126/science.287.5461.2185; RAMEDLINE-20196006; PubMed-10.7126/science.287.5461.2185; RAMEDLINE-20196006; PubMed-10.7126/science.287.5461.2185; RAMEDLINE-20196006; PubMed-10.7126/science.287.5461.2185; RAMEDLINE-2019600 R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D., Ramedon R.C., Rogers Y.-H.C., Blazel R.G., Molton C.R., Miklos G.L.G., RAMEDLI J. P., Agbayani A., An H.-J., Addrews-Frankoch C., Bladwin D., Ballew R.M., Baxendale J., Bayraktaroglu L., Beasley E.M., Benckova D., Botchan M.R., Bouck J., Benckov J., Botchan M.R., Bouck J., Benckov B.C., Duwenoo, C., Rockova D., Botchan M.R., Bouck J., Benckov B.C., Davenoor B., Botchan M.R., Bouck J., Benckov B.C., Davenoor B., Botchan M., Cawley S., Dahlke C., Davenoor B., Davids P., Ander M. Cawles P., Davids P., Ander M. Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferrac S., Plaischman W., Ralush P., Karngelista C.C., Ferrac C., Reraison J.A., Molton B., R., Houston R.A., Gong P., Gorirellan A.B., Gablart W.M., Glasser K., Ander M., Gabriellan A.B., Gabriellan A.B., Gabriellan A.B., Gabriellan A.B., Gabriellan A.B., Molton G.H., Ke Z., Kalp D., Lai Z., Liang Y., Lin X., Matteil B.E., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Matteil B., McIntosh T.C., McLeod M.P., Puris W., Molson D.L., Now M., Murphy B., Murphy L., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Murphy D., Weisenbach J., Spirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.-Y., Wassarman D.A., Wainstock G.M., Weisenbach J., Spirkas R., Zhong R., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zho
 MEDLINE-22456070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
 Celliker S. B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha; Ebhydroidea, Drosophilidae, Drosophila.
 01-MAY-2000, integrated into UniProtKB/TrEMBL
Q9VBP3 DROME PRELIMINARY; PRT; 1181 AA.
 Name=tankyrase; ORFNames=Dmel CG4719;
 MEDLINE=22426065; PubMed=12537568;
 07-PEB-2006, entry version 32.
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 NUCLEOTIDE SEQUENCE.
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 CG4719-PA.
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Distributed under the Creative Commons Attribution-NoDerivs License
 91 AAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEY
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MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Berkeley Drosophila Genome Project,
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
 'Annotation of the Drosophila melanogaster euchromatic genome: a
 Length 1181;
 GO; GO:0005634; C:nucleus; IEA.
GO; GO:000350; F:ND+ ADP-ribosyltransferase activity; IEA
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
InterPro; IER002110; ANK.
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 1181 AA; 127945 MW; EB6F0F94E6A3D504 CRC64;
 "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
 Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
 systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
 EMBL; AE003752; AAF56487.1; -; Genomic_DNA.
HSSP; P20749; 1K1B.
FlyBase; FBgn0027508; tankyrase.
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 KLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAE 1137
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Q9X237\_DROME PRELIMINARY; PRT; 1181 AA. 09X237. 09X237. 01-NOV-1999, integrated into UniProtKB/TrEMBL. 01-NOV-1999, sequence version 1. 07-FEB-2006, entry version 26.

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DROME

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 91 AAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEY
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 NUCLEOTIDE SEQUENCE.
Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
Celniker S.E.
 R HSSP; P20749; 1KIB.

R FlyBase; PB00027508; tankyrase.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R InterPro; IPR001210; PARP.

R InterPro; IPR001230; PARP.

R InterPro; IPR011231; PARP catalytic.

R InterPro; IPR011510; SAM.

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R SMART; SM00454; ANK; 15.

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Name-tankyrase; ORFNames-CG4719;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Length 1181;
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PROSITE; PSS0088; ANK REPEAT; 14.
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PROSITE; PSS0105; SAW DOMAIN; 1.
ANK repeat; Hypothetical protein; Repeat.
SEQUENCE 1181 AA; 127885 WW; 4E2BF31549BBA2D9 CRC64;
 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
 Query Match 61.8%; Score 3997; DB 2;
Best Local Similarity 65.2%; Pred. No. 2.4e-226;
Matches 771; Conservative 166; Mismatches 190;
 EMBL; AF132196; AAD34784.1; -; mRNA.
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RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Ramont C., Skalli Z., Cattolico L., Poulain J.-P., Gouzy J.,
Ramont C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Ralis M., Volff J.-N., Guigo R., Zody M.J., McEwan P., Bosak S.,
Ralis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Schachter Y., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II Nature 431:946-957(2004).

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1073
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EMBL, CAAE01014752, CAG04910.1; -; Genomic\_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003950; F:NAb- ADP-ribosyltransferase activity; IEA.
GO; GO:0003950; P:Nab- ADP-ribosyltransferase activity; IEA.
GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
InterPro; IPR012110; ANK.
InterPro; IPR012317; PARP\_catalytic.
Pfam; PF00053; ANK; 1.
Pfam; PF00644; PAKF; 1.

PROSITE; PS50297; ANK REP REGION; 1. PROSITE; PS50088; ANK REPEAT; 10. PROSITE; PS51059; PARP CATALYTIC; 1.

ANK repeat

SEQUENCE

PRINTS; PR01415; ANKYRIN. SMART; SM00248; ANK; 9.

Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FBB-2004) to the RBBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which

NUCLEOTIDE SEQUENCE

preliminary data.

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 248 GEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQH
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1047 1047
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 51.4%; Score 3324; DB 2; 60.5%; Pred. No. 9.1e-187; tive 73; Mismatches 135;
 Matches 682; Conservative
 Similarity
 340
 394
 Query Match
 78
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19-27/2 TETMG PRELIMINARY; PRT; 1047 AA.
C 048372.
T 19-40L-2005, integrated into UniProtKB/TrEMBL.
T 19-40L-2005, sequence version 1.
T 07-PBB-2006, entry version 5.
C hormosome 4 SCAFL4752, whole genome shotgun sequence. (Fragment).
B Chromosome 4 SCAFL4752, whole genome shotgun sequence. (Fragment).
C Tetraodon nigroviridis (Green puffer).
C Actinopterygii, Neopterygii; Teleostei; Buteleostomi;
C Actinopterygii, Neopterygii; Percomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
C Tetradontoidea; Tetraodontidae; Tetraodontiformes;
C NCBI\_TaxID=99883;

TETING

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Methods Enzymol. 303:19-44(1999)
 959 LGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYL 1018
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AC QBEXH7;
DT 01-MAK-2003, integrated into UniprotKB/TrEMBL.
DT 11-OCT-2005, sequence version 2.
DT 07-PEB-2006, entry version 18.
DF 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, DE clone:B930018021 product:TANKYRASE-RELATED PROTEIN homolog (Fragment).
CC EUKaryca; Merazoa; Chordata, Craniata; Vertebrata; Buteleostomi; CC Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; CC Murcidea; Muridae; Murinae; Mus.
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 Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

December 18, 2006, 17:34:55 Run on:

; Search time 41.423 Seconds (without alignments) 2620.235 Million cell updates/sec

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| c                   | 4, Appli | 4, Appil         | s, Appli<br>5, Appli                 | 26, Appl         | 3, Appli        | 3, Appli         | 9, Appli         | 2, Appli        | 10, Appl          | 4, Appli         | 2, Appli        | 2, Appli        | 8, Appli         | 2, Appli |                  | 10, Appl         | _                | 8, Appli         | 8, Appli        | 8, Appli        |                    | 6966, Ap           | _                  |            | 6965, Ap           |
|---------------------|----------|------------------|--------------------------------------|------------------|-----------------|------------------|------------------|-----------------|-------------------|------------------|-----------------|-----------------|------------------|----------|------------------|------------------|------------------|------------------|-----------------|-----------------|--------------------|--------------------|--------------------|------------|--------------------|
| Description         | Sequence | Sequence         | Sequence                             | Sequence         | Sequence        | Sequence         | Sequence         | Sequence        | Sequence          | Sequence         | Sequence        | Sequence        | Sequence         | Sequence | Sequence         | Sequence         | Sequence         | Sequence         | Sequence        | Sequence        | Sequence           |                    |                    | Sequence   | Sequence           |
| OUTTAKEES           | ! ? '    | US-U9-843-159B-4 | US-U9-9/2-II5A-6<br>US-09-350-982C-5 | US-09-849-602-26 | US-09-696-668-3 | US-09-843-159B-3 | US-09-843-159B-9 | US-09-427-154-2 | US-09-843-159B-10 | US-09-972-115A-4 | US-09-196-387-2 | US-09-841-835-2 | US-09-972-115A-8 |          | US-09-964-899-41 | US-09-196-387-10 | US-09-841-835-10 | US-09-843-159B-8 | US-09-196-387-8 | US-09-841-835-8 | US-09-949-016-6978 | US-09-949-016-6966 | US-09-949-016-6964 | -09-949-01 | US-09-949-016-6965 |
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| Length              | 1240     | 1240             | 1166                                 | 1227             | 1100            | 1100             | 1100             | 1100            | 1083              | 1267             | 1327            | 1327            | 1327             | 1333     | 802              | 949              | 949              | 583              | 673             | 673             | 4377               | 1719               | 1856               | 1880       | 1881               |
| &<br>Query<br>Match | 100.0    | 100.0            | 94.0<br>93.0                         | 90.9             | 89.2            | 89.2             | 89.1             | 88.7            | 87.5              | 84.3             | 79.0            | 79.0            | 79.0             | 77.8     | 6.09             | 51.2             | 51.2             | 45.1             | 33.0            | 33.0            | 13.8               | 13.6               | 13.6               | 13.6       | 13.6               |
| Score               | 6464     | 6464             | 6053                                 | 5877             | 5766            | 5766             | 5760             | 5731.5          | 2656              | 5452             | 5103.5          | 5103.5          | 5103.5           | 5031.5   | 3938             | 3307             | 3307             | 2913             | 2132.5          | 2132.5          | 892.5              | 878.5              | 878.5              | 878.5      | 878.5              |
| Result<br>No.       |          | 7                | n 4*                                 | S                | 9               | 7                | œ                | 6               | 10                | 11               | 12              | 13              | 14               | 15       | 16               | 17               | 18               | 19               | 20              | 21              | 22                 | 23                 | 24                 | 25         | 56                 |

| Sequence 9010, Ap                        | sequence 9012, Ap<br>Sequence 9013, Ap<br>Sequence 9014, Ap    | Sequence 9015, Ap<br>Sequence 9016, Ap<br>Sequence 9017, Ap    | Sequence 4, Appli<br>Sequence 4, Appli | Sequence 1246, Ap<br>Sequence 20, Appl  | Sequence 3, Appli<br>Sequence 3, Appli | Sequence 33, Appl<br>Sequence 33, Appl | Sequence 33, Appl<br>Sequence 33, Appl<br>Sequence 45196, A |
|------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------|-----------------------------------------|----------------------------------------|----------------------------------------|-------------------------------------------------------------|
| US-09-949-016-9010<br>US-09-949-016-9011 | US-09-949-016-9012<br>US-09-949-016-9013<br>US-09-949-016-9014 | US-09-949-016-9015<br>US-09-949-016-9016<br>US-09-949-016-9017 | US-09-172-977-4<br>US-09-404-108-4     | US-09-538-092-1246<br>US-09-972-115A-20 | US-09-172-977-3<br>US-09-404-108-3     | US-09-031-485-33<br>US-08-847-429A-33  | US-09-065-474-33<br>US-09-557-034-33<br>US-09-270-767-45196 |
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| 878.5                                    | 878.5<br>878.5<br>878.5                                        | 878.5<br>878.5                                                 | 877                                    | 877<br>874                              | 858<br>858                             | 835<br>835                             | 835<br>835<br>834.5                                         |
| 27                                       | 30 33 33 33 33 33 33 33 33 33 33 33 33 3                       | 332                                                            | 9 20                                   | 38<br>28                                | 39<br>40                               | 41                                     | 4 4 4<br>6 4 7                                              |

## ALIGNMENTS

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APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
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APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Nu, Xiang
APPLICANT: Huang, Betty
APPLICANT: August Betty
APPLICANT: Oseovakayar, Valeria
APPLICANT: Oseovakayar, Valeria
APPLICANT: Oseovakayar, Valeria
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APPLICANT: Oseovakayar, Valeria
TILLE OF INVENTION: TANKTRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS C
FILE REFERENCE: A-68292-1/RMS/DHR
CURRENT FILING DATE: 2002-07-23
PRIOR PILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/843,159B
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 1999-10-25
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Sequence 4, Application US/09843159B; Patent No. 6887675; GENERAL INFORMATION: APPLICANT: Chan, Evan APPLICANT: Chan, Evan; APPLICANT: Xu, Xiang; APPLICANT: Huang, Betty

US-09-843-159B-4

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794 720 854 780 1034

960

914 840 974 900

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1020
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 168
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 841 LDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRXLGLEHLMDIFEREQIT 900
 661 VKKLSSPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAA 720
 854
 914
 60 LRILIALILAVAAARIMSGRRCAGG-----GAACASAAABAVEPAARELFEACRN 108
 56
 721 SYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALXLAHGADPTLKNQEGQT
 1155 CPVHKDRSCYICHROLLFCRVTLGKSFLOFSAMKWAHSPPGHHSVTGRPSVNGLALAEYV
 12 QGAQRGARVGAA------HGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLL
 109 GDVERVKRLVTPEKVNSRDTAGRKSTPLHPAAGFGRKDVVBYLLQNGANVQARDDGGLIP
 SYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQT
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 LDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQIT
 975 LDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSP
 901 LDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSP
 1035 DDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIOKVCNKKLWERYTHRRKEVSEEN
 961 DDKEFQSVEBEMGSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEEN
 1095 HNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTG
 735 VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAA
 90.9%; Score 5877; DB 2; Length 1227; 91.6%; Pred. No. 0; ive 8; Mismatches 47; Indels 50.
 APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Petentin version 3.0
 1215 IYRGEQAYPEYLITYQIMRPEGMVDG 1240
 Sequence 26, Application US/09849602
Patent No. 6794501
GENERAL INFORMATION:
 Best Local Similarity 91.6
Matches 1148; Conservative
 r TYPE: PRT
ORGANISM: Homo sapiens
US-09-849-602-26
 US-09-849-602-26
 795
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 APPLICANT: Berthelsen, Jens
APPLICANT: Berthelsen, Jens
APPLICANT: Toma, Salvatore
APPLICANT: Isacchi, Matchella
TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Rela
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
FILE REPERENCE: PHRM-0043
CURRENT APPLICATION NUMBER: US/09/350,982C
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
 194
 61 PLHLAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFGHAEVVNLLLRHGADPNAR 120
 314
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 75 MSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKST
 1 MSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKST
 DNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDE
 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQL
 LOEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVS
 Gaps
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 Length 1166;
 9; Indels
 Match 93.6%; Score 6053; DB 2; Local Similarity 99.2%; Pred. No. 0; nes 1157; Conservative 0; Mismatches 9;
 NAME/KEY: misc feature

NAME/KEY: misc feature

NAME/KEY: misc feature

NAME/KEY: misc feature

COTHER INFORMATION: 0.1102)

OTHER INFORMATION: n is any nucleic acid

NAME/KEY: misc feature

LOCATION: (2650)

OTHER INFORMATION: n is any nucleic acid

US-09-350-982C-5
 Best Local Similarity 99.4
Matches 1157; Conservative
 LENGTH: 1166
TYPE: PRT
ORGANISM: Artificial
GENERAL INFORMATION:
 135
 121
 255
 181
 315
 375
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 435
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 421
 181
 675
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 Query Match
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COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (
 241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
 361 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWYY
 61 PIHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
 121 SGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
 ALHCAAAS PY PKRKQ I CELLLRKGAN I NEKTKEFLTPLHVAS EKAHNDVVEVVVKHEAKV
 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRD1EGRQSTPLHFAAGYNRVSVVEYLL
 LGNSEADROLLEAAKAGDVETVKKLCTVOSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL
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 141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLLRHGADPNARDNWNYT
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 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
 DB 2; Length 1100;
 Indels
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 Query Match
89.2%; Score 5766; Di
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 1; Mismatches
 Sequence 3, Application US/09696668
Patent No. 6617102
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Hang, Betty
APPLICANT: Hang, Betty
TILE OF INVENTION: TANKYRASE H, COMPOSITION
FILE REPERBNCE: A-68292-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/696,668
CURRENT FILING DATE: 2002-07-23
PRIOR PELING DATE: 1999-10-25
 SOFTWARE: PatentIn version 3.1
 NUMBER OF SEQ ID NOS: 11
 ; ORGANISM: Homo sapiens
US-09-696-668-3
 LENGTH: 1100
 621
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 SEQ ID NO 3
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 LKIQKVCNKKLMERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGM 1116
 SGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNI 1068
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 217 TDGRTALDLADPSAKAVLTGEYKKDELLESARSGNEEKNAMALLTPLNVNCHASDGRKSTP 276
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GDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIP 156
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 QSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEV
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 EKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLS
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 GDTDI QDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEV
 GDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEV
 AEYLLQHGADVNAQDKGGLI PLHNAASYGHVDVAALLI KYNACVNATDKWAFTPLHEAAQ
 757 AEYLLQHGADVNAQDXGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQ
 KGRTÓLCALLLAHGADPTLKNÓEGÓTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNG
 VRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGV
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 :
ENGTSPPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1227
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Gaps

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260 120 320 180 380 240 440 300 200 360 260 420 620 480 680 540 740 600 800 9

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121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180
 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
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 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFBREQITLDVLVE
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 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
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 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS
 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE
 SVEEEMOSTVREHRDGGHAGGIFNRYNILKIOKVCNKKLWERYTHRRKEVSEENHNHANE
 RMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD
 RSCYICHROLLFCRVTLGKSFLQFSAMKWAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ
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 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
 AYPEYLITYQIMRPEGMVDG 1240
 ; Sequence 9, Application US/09843159B; Betent No. 6887675; GENERAL INFORMATION:
 109
 961
 1021
 1221
 181
 1101
 1161
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 361
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 441
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 Sequence 3, Application US/09843159B
Patent No. 6887675
GENERAL INFORMATION:
APPLICANT: Luo, Yin
APPLICANT: Chan, Evan
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
CURRENT Huang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REFERENCE: A-6882-2.7KMS/DHR
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
 RSCYICHROLLFCRVTLGKSFLOFSAMKWAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1220
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 1041 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1100
 840
 780
 980
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 260
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 1 GFGRXDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGGTPLDLVS
 141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
 SPSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE
 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE
 Gaps
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 Length 1100
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 89.2%; Score 5766; Di
99.9%; Pred. No. 0;
ive 1; Mismatches
 AYPEYLITYQIMRPEGMVDG 1240
 AYPEYLITYQIMRPEGMVDG 1100
 Query Match
Best Local Similarity 99.9
Matches 1099; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-843-159B-3
 US-09-843-159B-3
 1221
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APPLICANT: Luo, Ying
APPLICANT: Luo, Ying
APPLICANT: Chan, Eva
APPLICANT: Chan, Eva
APPLICANT: Ku, Xiang
APPLICANT: Huang, Betty
TITLE OF INVENTION: TANKYRASE H, COMPOSTIONS INVOLVED IN THE CELL CYCLE AND
TITLE OF INVENTION: METHODS OF USE
TILE REPERENCE: A-68292-DJB/RMS/DAV
CURRENT PELING TANKYRASE: US/09/427,154
CURRENT PILING DATE: 1999-10-25
NUMBER OF SEQ. ID NOS: 9
 MGHKELKEIGINAYGHRHKLIKGVERLISGOQGLNPYLTLUTSGSGTILIDLSPDDKEFQ 1040
 1041 SVEBEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKCMERYTHRRKGVSEENHMHANE 1100
 1101 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1160
 260
 120
 320
 180
 380
 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAARBADVTRIKKHLSLEMVNFKHPQTHET 440
 9
 1 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
 861 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
 SPSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE
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 141 GFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
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 321 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
 721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
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 Gaps
 Query Match

88.7%; Score 5731.5; DB 2; Length 1100;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1095; Conservative 1; Mismatches 3; Indels 1;
 1081 AYPEYLITYOIMRPEGMVDG 1100
 1221 AYPEYLITYQIMRPEGMVDG 1240
 ; Sequence 2, Application US/09427154; Patent No. 6589725
 Patentin Ver. 2.1
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-427-154-2
 GENERAL INFORMATION:
 LENGTH: 1100
 -09-427-154-2
 381
 SOFTWARE:
SEQ ID NO 2
 981
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APPLICANT: Chan, Evan
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
APPLICANT: Huang, Beetty
TITLE CNNT: Huang, Beetty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REFERENCE: A-68292-2/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/843,159B
CURRENT FILING DATE: 2001-04-25
PRIOR PILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR PILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 17
SEQ ID NO SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 1100
 ö
 240
 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADFTLKNQEGQTPLDLVS 860
 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 260
 SGNEEKWMALLIPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 320
 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 440
 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 500
 361 NALDNIGGTSLHRAAYCGHLQTCRILLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420
 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
 9
 141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 200
 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60
 PLHNACSYGHYEVTELLVKHGACYNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
 NALDNIGQTSLHRAAYGGHLQTCRLLLSYGCDPNI ISLQGFTALQMGNENVQQLLQBGIS
 OHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
 1 CKLLLQHGADPTKKNRDGNTPLDLVKDGDTD1QDLLRGDAALLDAAKKGCLARVKKLSS
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 Query Match 89.1%; Score 5760; DB 2; Length 1100; Best Local Similarity 99.8%; Pred. No. 0; Matches 1098; Conservative 1; Mismatches 1; Indels 0
 OTHER INFORMATION: synthetic mutant
 TYPE: PRT
ORGANISM: Artificial sequence
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 SPSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 980
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 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV
 241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
 ADDVSALLTAAMPPSALPSCYKPQVINGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
 ADDVSALLTAAMPPSALPSCYKPQVINGVRSPGATADALSSGPSSPSSLSAASSLDNLSG
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 141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT
 1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWYYT
 201 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR
 ALHCAAAS PY PKRKOICELLLRKGANINEKTKEFLT PLHVASEKAHNDVVEVVVKHEAKV
 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL
 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL
 NCHNKSAI DLA PT PQLKERLA Y EFKGHSLLQAAREADVTRIKKHLSLEMVN FKH PQTHET
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 Score 5656; Di
Pred. No. 0;
1; Mismatches
 , OTHER INFORMATION: synthetic mutant
US-09-843-159B-10
PRIOR PILLING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 09/
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 1083
 ORGANISM: Artificial sequence
 Query Match
Best Local Similarity 99.8%;
Matches 1079; Conservative
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 Methoda
 Sequence 10, Application US/09843159B
Patent No. 6897675
GENERAL INPORMATION:
APPLICANT: Luo, Yin
APPLICANT: Chan, Evan
APPLICANT: Chan, Evan
APPLICANT: Huang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and N
FILE REFERENCE: A-68292-2/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/843,159B
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/696,668
 -SCYICHRQLLFCRVTLGKSFLQPSAMKWAHSPPGHHSVTGRPSVNGLALAEVVIYRGEQ 1079
 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 1040
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 241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300
 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
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 SFSELSSLVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE
 SVEEEMOSTVREHRDGGHAGGIFNRYNILKIOKVCNKKLWERYTHRRKEVSEENHNHANE
 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVGIGGGTGCPVHKD
 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE
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 PDNVNCRDTGGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD
 VAALLI KYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS
 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGGTPLDLVS
 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE
 RSCYI CHROLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVI YRGEQ
 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL
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 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITOFVRNLGLEHLMDIFEREQITLDVLVE
 AYPEYLITYQIMRPEGMVDG 1240
 US-09-843-159B-10
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us-10-616-101-4.rai

| LOCATION: (166)(166)  OTHER INFORMATION: The NAMB/KEY: misc feature i.COATION: (173)(173)(173)(173)(173)(173)(173)(173)(173)(173)(173)(173)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(174)(1 | LOCATION: (227). (227)  INDER INPORMATION: The NAME/KEX: misc feature incation: (228). (228)  OTHER INFORMATION: The NAME/KEX: misc feature incation: (237). (237). (237). (237). (237). (237). (237). (237). (237). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). (238). |
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| 991 WGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLATSGSGTILIDLSPDDKEPQ 1040                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 'Xaa' at location 1 stands for Thr, Ala, Pro, or Ser. 'Xaa' at location 42 stands for Lys, Arg, Thr, or Met. 'Xaa' at location 10 stands for Thr, Ala, Pro, or Ser. 'Xaa' at location 114 stands for Thr, As, Ser, Thr, or Ile. 'Xaa' at location 126 stands for Lys, or Asn. 'Xaa' at location 139 stands for Ile, Val, Leu, or Phe. 'Xaa' at location 153 stands for Thr. 'Xaa' at location 153 stands for Thr.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| OY  981 MGHKELKEIGINAYGHRHKLIKGV  B41 MGHKELKEIGINAYGHRHKLIKGV  OY  1041 SVEEEMQSTVREHRDGGHAGGIFN  105 SVEEEMQSTVREHRDGGHAGGIFN  106 SVEEEMQSTVREHRDGGHAGGIFN  OY  1101 RMLFHGSPFVNAIIHKGFDERHAY  OY  1101 RMLFHGSPFVNAIIHKGFDERHAY  OY  1101 RMLFHGSPFVNAIIHKGFDERHAY  OY  1101 RMLFHGSPFVNAIIHKGFDERHAY  OY  1101 RMLFHGSPFVNAIIHKGFDERHAY  OY  1121 A 121  Db  1021 RSCYICHRQLLFCRVTLGKSFLQF  OY  1221 A 1221  Db  1081 A 1081  Db  1081 A 1081  APPLICATION  SEGQUAN  GEGGG, MOTIN B.  APPLICANT: Geregg, Morin B.  APPLICANT: Malter, Funk D.  APPLICANT: Malter, Funk D.  APPLICANT: Malter, Funk D.  APPLICANT: Malter, Funk D.  APPLICANT: Malter, Funk D.  APPLICANT: Malter, Funk D.  TITLE OF INVENTION: A Second Mammal FILE OF INVENTION: A Second Mammal FILE OF INVENTION NUMBER: US 60/129  PRIOR PRIOR APPLICATION NUMBER: US 60/129  PRIOR PILING DATE: 2000-04-10  PRIOR PILING DATE: 2000-04-13  NUMBER OF SEQ ID NOS: 64  NUMBER OF SEQ ID NOS: 64  NUMBER OF SEQ ID NOS: 64                                                                                                                                                                                                                                                                                                                                                                                        | LENGTH: 1267  TYPE: PRT  ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc feature LOCATION: (1)(1) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (42)(42) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (98)(98) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (110)(110) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (114)(114) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (1145)(1139) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (1145)(1139) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (1139)(139) OTHER INFORMATION: The NAME/KEY: misc feature LOCATION: (1144)(1441) NAME/KEY: misc feature LOCATION: (1153)(153) OTHER INFORMATION: The NAME/KEY: misc feature                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

'Xaa' at location 215 stands for Lys, Asn, Glu, Asp, Gln, His stop codon, or Tyr. le 'Xaa' at location 238 stands for Asn, Ser, Thr, Ile, Asp, Gly Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe. 'Xaa' at location 667 stands for Tyr, Cys, Ser, or Phe. 'Xaa' at location 727 stands for His, Arg, Pro, or Leu. 'Xaa' at location 173 stands for Ile, Val, Leu, or Phe. 'Xaa' at location 188 stands for Asn, Asp, His, or Tyr. 'Xaa' at location 207 stands for Asn, Asp, His, or Tyr. 'Xaa' at location 211 stands for Gln, Arg, Pro, or Leu. 'Xaa' at location 213 stands for Ser, Gly, Arg, or Cys. 'Xaa' at location 228 stands for Asn, Asp, His, or Tyr. e 'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys. 'Xaa' at location 185 stands for Thr, Ala, Pro, or Ser. 'Xaa' at location 205 stands for Asn, Ser, Thr, or Ile. 'Xaa' at location 227 stands for His, Arg, Pro, or Leu. ie 'Xaa' at location 764 stands for Tyr, Cys, Ser, or Phe. e 'Xaa' at location 741 stands for Met, Val, or Leu. 'Xaa' at location 204 stands for Glu, or Lys. 'Xaa' at location 725 stands for Lys, or Asn. e 'Xaa' at location 763 stands for Leu, or Phe. 'Xaa' at location 174 stands for Glu, or Lys. 'Xaa' at location 202 stands for His, or Pro. 'Xaa' at location 735 stands for Glu, or Asp. 'Xaa' at location 237 stands for Glu, or Asp. 'Xaa' at location 183 stands for Val.

| ; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, ; AME/KEY: misc feature; NAME/KEY: misc feature; LOCATION: (802) (802)  Query Match                                                                                                                                                                                                                                                                                                                              | Qy         121 EKVNSRDTAGRKSTPLHFRAAGFGRKDVVEYLLONGANVQARDDGGLIPLHNACSFGHAEV         180           Db         146 EKVNSRDXAGRKSTPLHFPAXFGRKDLXXYLLTNGANXQXRDXGGLIPLHNACSFGXAXX         205           Qy         181 VALLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADP         240           ENTLLKHXAXFNARDNWNYTPKXEAAIKGKIXXCIVLQHGAEPTIRNTDGRTALDLADP         265           Qy         241 SAKAVLTGEYKKDELLESARSGNEEKWAALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI         300           Qy         265 SAKAVLTGEYKKDELLESARSGNEEKWAALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI         325           Qy         301 VQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAAS         360           QY         101 LLLLLHAAGYNGKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAAS         360 | Db 326 VQLLLQHGADVHAKDKGBLVPLHNACSYGHYEVTELLVKHGACVNAMDLMQFTPLHEAAS 385  Qy 361 KNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTR 420                                                                                                                                                                                                                                                                                    | GY         541 FTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQ         600           B         566 FTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQ         625           GY         601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVN         660           BD         626 STPLHFAAGXNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVN         685           GY         661 VADLWKFTPLHEAAAKGKYEICKLLLQHGADVHAKDGGLVPLHNACXYGHYEVAELLVKHGANVN         685           GY         661 VADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKKKKRGXIXLDLVKDGTDIQDLLRGD         720           B         686 VADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKKKKGXIXLDLVKDGXTDIQDXLRGD         745           CV         721 AALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEXTLQHGADVN         780 |                                                                                                                                                                                                                                                                                                                                                                                   |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Lye, Asn, Arg, Ser, Thr, Ile His, Pro, Leu, a stop codon, Lye, Asn, Arg, Ser, Thr, Ile His, Pro, Leu, a stop codon, Lye, Asn, Arg, Ser, Thr, Ile His, Pro, Leu, a stop codon,                                                                                                                                                                                                                                                                                                                           | Arg, Ser, Thr, Ile<br>Leu, a stop codon,<br>Arg, Ser, Thr, Ile<br>Leu, a stop codon,<br>Arg, Ser, Thr, Ile<br>Leu, a stop codon,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Lys, Asn, Arg, Ser, Thr, Ile His, Pro, Leu, a stop codon, Lys, Asn, Arg, Ser, Thr, Ile His, Pro, Leu, a stop codon, Lys, Asn, Arg, Ser, Thr, Ile His, Pro, Leu, a stop codon,                                                                                                                                                                                                                                                       | Asn, Arg, Ser, Thr, lle Pro, Leu, a stop codon, Asn, Arg, Ser, Thr, lle Pro, Leu, a stop codon, Asn, Arg, Ser, Thr, lle                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | odon,<br>Ile<br>odon,<br>Ile                                                                                                                                                                                                                                                                                                                                                      |
| NAME/KEY: misc feature LOCATION: (787)(787) OTHER INFORMATION: The 'Xaa' OTHER INFORMATION: "Met, Glu OTHER INFORMATION: Trp, Trp, NAME/KEY: misc feature LOCATION: (788)(788) OTHER INFORMATION: The 'Xaa' OTHER INFORMATION: "Met, Glu OTHER INFORMATION: "Met, Glu OTHER INFORMATION: "Met, Glu OTHER INFORMATION: "Met, Glu OTHER INFORMATION: The 'Xaa' OTHER INFORMATION: "Met, Glu OTHER INFORMATION: The 'Xaa' OTHER INFORMATION: The 'Xaa' OTHER INFORMATION: Try, Trp, NAME/KEY: misc_feature | LOCATION: (790). CTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: Tyr, '] NAME/KEY: Misc feature LOCATION: (791). (791) OTHER INFORMATION: The ') OTHER INFORMATION: 'Met, OTHER INFORMATION: 'Y' NAME/KEY: Misc feature LOCATION: (792). (792) OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ')                                                                                                                                                                                                                                                                                                                                                   | MAMEATION: (1931)(1931) OTHER INFORMATION: The ') OTHER INFORMATION: Met, OTHER INFORMATION: Tyr, NAME/KEY: Misc feature LOCATION: (1941)(1943) OTHER INFORMATION: The ') OTHER INFORMATION: Tyr, NAME/KEY: Misc feature LOCATION: (1955)(1953) OTHER INFORMATION: Tyr, OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') OTHER INFORMATION: The ') | OTHER INFORMATION: 177,  NAME/KEY: misc feature LOCATION: (7967(796) OTHER INFORMATION: The OTHER INFORMATION: The LOCATION: (797)(797) OTHER INFORMATION: The LOCATION: (797)(797) OTHER INFORMATION: Met, OTHER INFORMATION: Met, OTHER INFORMATION: The OTHER INFORMATION: Met, OTHER INFORMATION: The OTHER INFORMATION: The OTHER INFORMATION: The OTHER INFORMATION: The OTHER INFORMATION: The OTHER INFORMATION: (798)                                                                                                                                                                                                                                                                                                                                                                          | OTHER INFORMATION: , Met OTHER INFORMATION: 17r, NAME/KEY: misc feacure LOCATION: (799](799) OTHER INFORMATION: The OTHER INFORMATION: Tyr, OTHER INFORMATION: Tyr, INFORMATION: (800) OTHER INFORMATION: , Met OTHER INFORMATION: Tyr, NAME/KEY: misc feature LOCATION: (801) (801) OTHER INFORMATION: Tyr, NAME/KEY: misc feature LOCATION: (801) (801) OTHER INFORMATION: Tyr, |

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 LEHLMD I FXREQITLDVLVEMGHKELKEIXINAYGHRHKLIKSFERLISGQQGLNPYLTL
 :
RHEERYTHRRKEVSEENHNHANBRRMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAE
 NSSKSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHH
LEHLMDI FEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGOOGLNPYLTL
 NTSGSGTILIDLSPDDKEPQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNK---
 KLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAE
 NSSKSNQYVYG1GGGTGCPVHKDRSCY1CHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHH
 22 AAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLALLLAVAAARIMSGRRCA
 15;
 APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDESE: 12
CORRESPONDESES: 31
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
 SVTGRPSVNGLALAEVVIYRGEQAYPEYLITYQIMRPEGMVDG 1240
 Query Match 79.0%; Score 5103.5; DB 2; Length Best Local Similarity 79.2%; Pred. No. 0; Matches 963; Conservative 110; Mismatches 128; Indels
 SUFTWARE: Patentin PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING PATE:
CLASCY-DATE:
 CIP1
 600-1-230
 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
 09/095,225
 Sequence 2, Application US/09196387
Patent No. 6277613
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy, disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
SOFTWARE: PatentIn Release #1
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A
 TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1327 amino acids
 STRANDEDNESS: single
TOPOLOGY: linear
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 STREET: 411 Hacken
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 amino acid
 GENERAL INFORMATION:
 CLASSIFICATION:
 US-09-196-387-2
 US-09-196-387-2
 1045
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1159 SAAGVAPNPAGSGSNNSPSSSSSPTSSSSSPSSPG----SSLAESPEAAGVSTAPL 165 285 201 261 321 405 381 465 441 525 501 585 561 621 705 681 765 741 825 801 861 945 921 998 979 226 FGRKDVVEHLLQMGANVHARDDGGLIPLHNACSFGHAEVVSLLLCQGADPNARDNWNYTP GNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVP 346 GNEEKLMALLTPLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLLQHGADVHAKDKGGLVP 406 LHNACSYGHYEVTELLLKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLVN ALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGISL 646 RISDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYNRVSVVEYLLH 766 CKLLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLKGDAALLDAAKKGCLARVQKLCTP 742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV 802 AALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSA ERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHK **GGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAG** FGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTP LHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESARS LHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN CHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETA LHCAAAS PY PKRKQ I CELLLRKGAN I NEKTKE FLT PLHVAS EKAHNDVVEVVVKHEAKVN 586 ALDTLGQTALHRAALAGHLQTCRLLLSYGSDPSIISLQGFTAAQMGNEAVQQILSESTPI GNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDI EGRQSTPLHFAAGYNRVSVVEYLLQ CKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSP 862 DDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGS **OSVEEEMOSTVREHRDGGHAGGIFNRYNILKIOKVCNKKLWERYTHRRKEVSEENHNHAN** HGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEI EMCHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEF

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346 GNEEKLMALLTPLINVNCHASDGRKSTPLHLAAGYNRVRIVQLLLQHGADVHAKDKGGLVP
 406 LHNACSYGHYEVTELLLKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLVN
 562 GNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLO
 286 LHEAAIKGKIDVCIVLLOHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARS
 LHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN
 502 ALDNIGOTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGISL
 766 CKLLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLKGDAALLDAAKKGCLARVQKLCTP
 DNVNCRDTQGRHSTPLHLAAGYNNLEVABYLLQHGADVNAQDKGGLIPLHNAASYGHVDV
 862 DDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGS
 922 FSELSSVVSSSGTEGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLV
 1040 OSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHAN
 1160 DRSCYICHROLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGE
 CHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETA
 LHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVN
 706 HGADVHAKDKGGLVPLHNACSYGHYEVAELLVRHGASVNVADLWKFTPLHEAAAKGKYEI
 682 CKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSP
 980 EMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEF
 ERMLFHGSPFVNAI IHKGFDERHAY IGGMFGAGI YFAENSSKSNOYVYGIGGGTGCPVHK
 622 HGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEI
 1220 QAYPEYLITYQIMRPE 1235
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1179 ERMLFHGSPFINAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPTHK 1238
 1239 DRSCYICHROMLFCRVTLGKSFLQFSTMMMAHAPDGHHSVIGRPSVNGLAYAEYVIYRGE 1298
 225
 201
 285
 112 SAAGVAPNPAGSGSNNSPSSSSSPTSSSSSPSSPG----SSLAESPEAAGVSSTAPL
 FGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLLRHGADPNARDNWYTP
 FGRKDVVEHLLQMGANVHARDDGGLIPLHNACSFGHAEVVSLLLCQGADPNARDNWYTP
 82 GGGAACASAAAEAVEPAARELPEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAG
 AAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLALLLAVAAARIMSGRRCA
 Gaps
 15;
 Length 1327
 RESULT 13
US-09-841-835-2
Sequence 2, Application US/09841835
Sequence 2, Application US/09841835
Sequence 2, Application US/09841835
Sequence 3, Application US/09841835
TITLE OF INVENTION:
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klaubex & Jackson
ADDRESSEE: Klaubex & Jackson
 Query Match
Best Local Similarity 79.2%; Pred. No. 0;
Matches 963; Conservative 110; Mismatches 128; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERRENCE/POCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
 ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 QAYPEYLITYQIMKPE 1314
 QAYPEYLITYQIMRPE 1235
 TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acide
 STRANDEDNESS: single
TOPOLOGY: linear
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 amino acid
 ZIP: 07601
 US-09-841-835-2
 22
 142
 226
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1)
OTHER INFORMATION: The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
OTHER INFORMATION: yr, Trp, Cys, or Phe.
LOCATION: (2)...(2)
 APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Gregg, Morin B.
APPLICANT: Matler, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SSCTWARE: PatentIn version 3.1
SEQ ID NO.
 Sequence 2, Application US/09972115A Patent No. 6599728 GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 US-09-972-115A-2
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 226 FGRXDVVEHLLQMGANVHARDDGGLIPLHNACSFGHAEVVSLLLCQGADPNARDNWYYF 285
 345
 406 LHNACSYGHYEVTELLLKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLVN 465
 585
 166 GPGAAGPGTGVPAVSGALRELLEACRNGDVSRVRRLVDAANVNAKDMAGRKSSPLHFAAG 225
 201
 321
 LHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN 381
 CHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETA 441
 LHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVN 501
 561
 621
 681
 706 HGADVHAKDKGGLVPLHNACSYGHYEVAELLVRHGASVNVADLWKFTPLHEAAAKGKYEI 765
 LHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESARS 261
 586 ALDTLGOTALHRAALAGHLOTCRLLLSYGSDPSIISLQGFTAAQMGNEAVQQILSESTPI
 GGGAACASAAABAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAG
 FGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTP
 GNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVP
 ALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGISL
 562 GNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQ
 HGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEI
 22 AAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLALLLAVAAARIMSGRRCA
 15; Gaps
 Query Match 79.0%; Score 5103.5; DB 2; Length 1327; Best Local Similarity 79.2%; Pred. No. 0; Matches 963; Conservative 110; Mismatches 128; Indels. 15;
 GENERAL INCORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
FRIOR APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
SECOND OF TRICKS OF
 Sequence 8, Application US/09972115A
Patent No. 6599728
 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-972-115A-8
 142
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980 EMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEF 1039
741
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 998
 979
 886 AALLIKYNTCVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTMKNQBGQTPLDLATA
 862 DDVSALLTAAMPPSALPSCYKPQVINGVRSPGATADALSSGPSSPSSLSAASSLDNLSGS
 922 FSELSSVVSSSGTEGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLV
 1040 OSVEEEMOSTVREHRDGGHAGGIFNRYNILKIOKVCNKKLWERYTHRRKEVSEENHNHAN
 1100 ERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHK
 1179 ERMLFHGSPFINAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPTHK
682 CKLILIQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSP
 742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDV
 802 AALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSA
 1220 QAYPEYLITYQIMRPE 1235
 1299 QAYPEYLITYQIMKPE 1314
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| ; NAME/KEY: misc_feature<br>; LOCATION: (17)(17)<br>; OTHER INFORMATION: The 'Xaa' at location 17 stands for Lys, Asn, Arg, Ser, Thr, Ile,<br>; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,<br>; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.<br>; NAME/KEY: misc_feature | ; LOCATION: (18)(18) ; OTHER INFORMATION: The 'Xaa' at location 18 stands for Lys, Asn, Arg, Ser, Thr, Ile, ; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro; Leu, a stop codon, ; OTHER INFORMATION: Tyr, Trp, Cys, or Phe. ; NAME/KRY: misc feature | COCATION: (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (19) (1 | ; LOCATION: (20)(20) ; OTHER INFORMATION: The 'Xaa' at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile, ; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, ; OTHER INFORMATION: Tyr, Trp, Cys, or Phe. | NAME/KBY: misc feature  JOCATION: (21)-(21)  OTHER INFORMATION: The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe. | <ul> <li>MARIO AZII INISC. LEGILUIE</li> <li>INCORTION: (22)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(52)(</li></ul> | ORMAT<br>ORMAT<br>ORMAT<br>misc                  | <ul> <li>JOCATION: (24) (24)</li> <li>OTHER INFORMATION: The 'Xaa' at location 24 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.</li> <li>NAME/KEY: misc facture</li> <li>TORMITON: (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25) (25)</li></ul> | CTHER INFORMATION: The 'Xaa' at location 25 stands for Lys, Asn, Arg, Ser, Thr, Ile, CTHER INFORMATION: The 'Xaa' at location 25 stands for Lys, Pro, Leu, a stop codon, CTHER INFORMATION: Tyr, Trp, Cys, or Phe. Sharing Mark/KRY misc feature for the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the common control of the | ; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Asn, Arg, Ser, Thr, Ile,; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Pro, Leu, a stop codon,; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.; NAME/KEY: misc feature; Cat. feature (27) | 'Xaa' at location 27 stands for Lys, Asn, Arg, Ser, Thr,<br>Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codd<br>Trp, Cys, or Phe. | INFORMATION: The 'INFORMATION: Met, INFORMATION: Tyr, KEY: misc_feature (KEY: misc_feature): INFORMATION: The 'INFORMATION: Met, 'INFORMATION: Met, 'INFORMATION: Met, | ; OTHER INFORMATION: Tyr, Trp, Cys, or Phe. ; NAME/KEY: misc_feature ; LOCATION: (30) (30) ; OTHER INFORMATION: The 'Xaa' at location 30 stands for Lys, Asn, Arg, Ser, Thr, Ile, ; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, ; OTHER INFORMATION: Tyr, Trp, Cys, or Phe. | KEY: misc feature<br>ION: (31)(31)<br>INFORMATION: The 'Xaa' |
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| INFORMATION: The INFORMATION: Met, INFORMATION: Yr, KEY: misc. feature ION: (3). (3). (10) INFORMATION: The                                                                                                                                                                                                   | Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a st.<br>Ys, or Phe.<br>at location 4 stands for Lys. Man. Mrd. Ser.                                                                                                                                                          | Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a str. Trp, Cys, or Phe. Xaa' at location 5 stands for Lys, Asn, Arg, Ser,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop cor<br>Trp, Cys, or Phe.                                                                                                                                                                 | Xaa' at location 6 stands for Lys, Asn, Arg, Ser, Thr, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop coo'rp, Cys, or Phe.                                                                                                                                                                                                                     | OTHER INFORMATION: The 'Xaa' at location ' Beands for Lys, Ash, Arg, Ser, Int, Lie, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T OTHER INFORMATION: Yr, Trp, Cys, or Phe.  LOCATION: (8)(8)  OTHER INFORMATION: The 'Xaa' at location 8 stands for Lys, Asn, Arg, Ser, Thr, Ile,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | l, Gin, HiB, PrO, Leu,<br>1d8 for LyB, Asn, Arg, | Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a st Irp, Cys, or Phe.  Xaa' at location 10 stands for Lys, Asn, Arg, Ser                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Cys, or Phe.  at location 11 stands for Lys, Asn, Arg, Ser,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Trp, Cys, or Phe.  'Xaa' at location 12 stands for Lys, Asn,                                                                                                                                                                                                      | Trp, Cys, or Phe.  'Xaa' at location 13 stands for Lys, Asn, Arg, Ser, Glu, Asp, Glv, Ala, Val, Glu, His, Pro, Leu, a ston                | yr, Trp, Cys, or Phe.  re he 'Xaa' at location 14 stands for Lys, Asn, Arg, Ser, Tet, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop yr, Trp, Cys, or Phe.        | , Xaa,<br>Glu,<br>, Trp,                                                                                                                                                                                                                                                                                           | ORMAT<br>ORMAT<br>ORMAT                                      |

| Qy 774 QHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQ 833  Db 860 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX                                                                                                                                                                                                                                                                                                                   | 0y 894 ATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSIT 953                                                                                                                                                                                                                                                                                                                                                          | 1014 INPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQK 1100 INPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQK 1107 VCNKKLWERYTHRRKEVSEENHNHANERMIFHGSPFVNAIIHKGFDERHAYIG | 1160 VCNXXXXAKIRHEERYTHRRKEVSBENHNHANERMLFHGSPFVNAIIHKGFDERHAYIG 1127 GMPGAGIYFAENSSKSNQYYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSA | Db 1220 GMFGAGIYFFENSSKSNOYVYGIGGGTGCPVHKDRSCYICHROLLFCRVTLGKSFLGFSA 1279  Oy 1187 MKWAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLLTYQIMRPEGMVDG 1240  Db 1280 MKWAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLLTYQIMRPEGMVDG 1333                                                 | Search completed: December 18, 2006, 17:37:14<br>Job time : 46.423 secs. |                                                                         |                                                                         |                                                                         |                                                                             |                                                                         |                                                                         |                                                                             |                                                                         |                                                                       |
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| OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.  NAME/KEY: misc. feature LOCATION: (32)(32) OTHER INFORMATION: The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: The Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.  NAME/KEY: misc. feature LOCATION: (33)(33) | OTHER INFORMATION: The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.  NAME/KEY: misc feature LOCATION: (34) OTHER INFORMATION: The 'Xaa' at location 34 stands for Lys, Asn, Arg, Ser, Thr, Ile, OTHER INFORMATION: Met. Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon. | Trp, Cys, or Phe.  (aa' at location 35 stands for Lys, Asn, Arg, Strp, Cys, or Phe.                                                                                                            | NAME/KEY: misc_feature LOCATION: (36) (36) OTHER INFORMATION: The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile,   | Cucal Similarity 86.7%; Pred. No. 0; Deligin 1935; Matches 983; Conservative 7; Mismatches 135; Indels 9; Gaps 2;  Qy 116 RLVTPEKVNSRDTAGRKSTPLHFAAGFGRKOVVEYLLONGANVQARDGGLIPLHNACSF 175  Db 200 RLVTPEKVNXXNTXGRKSTPLHFPAGFGRKOXXXKYLLQNGANXQXLYNGGLIPLHXACSF 259 | Qy 176 GHAEVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTAL 235  | Qy 236 DLADPSAKAVLTGEYKKDELLESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGY 295 | QY 296 NRVKIVOLLLOHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLMOFTPL 355 | QY 356 HEAASKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEFKGHSLLQAARE 415 | OY 416 ADVTRIKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFL 475<br> | OY 476 TPLHVASEKAHNDVVEVVVKHEAKVNALDNLGGTSLHRAAYCGHLQTCRLLLSYGCDPNI 535 | OY 536 ISLOGETALOMGNENVOQLIQEGISLGNSEADROLLEAARAGDVETVKKLCTVQSVNCRD 595 | OY S96 IEGROSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKH 655<br> | GY 656 GAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKONDGNTPLDLVKDGDTDIQD 715 | QY 716 LIRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLL 773 |

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Sequence 629, App
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Sequence 1122, Ap
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 December 18, 2006, 17:55:21 ; Search time 40.3471 Seconds
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-371-354-56501

US-11-373-615-56

US-11-317-329-34

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US-11-317-354-78800
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

 Gapop 10.0 , Gapext 0.5
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Match Length DB
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 Perfect score:
Sequence:
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 Score
 OM protein
 Searched:
 Database
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| 26 392.5 6.1 784 7 US-11-317-329-12 Sequence 12, Appl 29 390.5 6.0 786 7 US-11-317-329-35 Sequence 13, Appl 29 390.5 6.0 786 7 US-11-317-329-31 Sequence 13, Appl 30 390.5 6.0 786 7 US-11-317-329-31 Sequence 31, Appl 30 390.5 6.0 786 7 US-11-317-329-31 Sequence 31, Appl 31 390.5 6.0 786 7 US-11-317-329-32 Sequence 32, Appl 32 382 5.9 766 6 US-10-602-394-94 Sequence 33, Appl 33 381.5 5.9 1765 6 US-10-602-394-94 Sequence 34, Appl 35 372.5 5.8 1735 6 US-10-602-394-91 Sequence 91, Appl 37 372.5 5.8 1771 6 US-10-502-394-91 Sequence 91, Appl 37 372.5 5.8 1777 6 US-10-502-394-91 Sequence 91, Appl 39 371.5 5.7 347 7 US-11-317-329-30 Sequence 91, Appl 41 370 5.7 175 6 US-10-502-394-89 Sequence 30, Appl 42 368.5 5.7 2278 6 US-10-502-394-89 Sequence 30, Appl 44 353.5 5.5 180 6 US-10-374-780A-1842 Sequence 1842, Appl 44 353.5 5.5 1180 6 US-10-374-780A-1842 Sequence 1977, Appl 44 353.5 5.5 1180 6 US-10-505-328-177 Sequence 1777, Appl 44 353.5 5.5 1180 6 US-10-505-328-177 Sequence 202, Appl 45 332.5 5.1 835 7 US-11-377-316-202 Sequence 202, Appl 45 332.5 5.1 835 7 US-11-377-316-202                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                      |                                      | ya.                                  | • •                                     |                  | •                |                  |                   |                  |                  |                  |                     |                     |                   |                   |            |
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| 392.5 6.1 784 7 US-11-317-329-12 Sequence 392.5 6.0 86 7 US-11-317-329-13 Sequence 390.5 6.0 786 7 US-11-317-329-31 Sequence 390.5 6.0 786 7 US-11-317-329-31 Sequence 390.5 6.0 786 7 US-11-317-329-32 Sequence 382 5.9 7762 6 US-10-502-394-94 Sequence 381.5 5.9 776 6 US-10-502-394-94 Sequence 372.5 5.8 1184 6 US-10-502-394-91 Sequence 372.5 5.8 1771 6 US-10-502-394-91 Sequence 372.5 5.8 1777 6 US-10-502-394-91 Sequence 372.5 5.8 1777 6 US-10-502-394-91 Sequence 372.5 5.8 1777 6 US-10-502-394-91 Sequence 372.5 5.8 1777 6 US-10-502-394-91 Sequence 372.5 5.8 1777 6 US-10-502-394-91 Sequence 372.5 5.8 1777 6 US-10-502-394-91 Sequence 370 5.7 7 US-11-317-329-30 Sequence 370 5.7 7 US-11-317-329-30 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-994-89 Sequence 370 5.7 1715 6 US-10-502-9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Appl<br>Appl                         | App1<br>App1                         | Appl<br>Appl                         | Appl<br>92. A                           | Appl             | Appl             | Appl             | , App             | Appl             | Appl             | Appl             | 2, Ap               | 77, A               |                   |                   |            |
| 392.5 6.1 784 7 US.11-317-329-12 390.5 6.0 786 7 US.11-317-329-13 390.5 6.0 786 7 US.11-317-329-13 390.5 6.0 786 7 US.11-317-329-13 390.5 6.0 786 7 US.11-317-329-33 382 5.9 786 7 US.11-317-329-33 381.5 5.9 776 6 US.10-502-394-94 380.5 5.9 777 6 US.10-502-394-91 372.5 5.8 1775 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-502-394-91 372.5 5.8 1777 6 US.10-504-973-30 372.5 5.8 1777 6 US.10-504-973-30 372.5 5.8 1777 6 US.10-504-973-30 372.5 5.7 2778 6 US.10-374-780A-1842 373.5 5.7 2278 6 US.10-374-780A-1842 357.5 5.5 180 6 US.10-374-7316-202                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 12,<br>96,                           | 31,                                  | 32,                                  | 94,                                     | 93,              |                  | 17,              |                   |                  | 89,              | 30,              | 184                 | 618                 | 177               | 202               |            |
| 392.5 6.1 784 7 392.5 6.1 392.5 6.1 832 7 390.5 6.0 786 7 390.5 6.0 786 7 390.5 6.0 786 7 390.5 6.0 786 7 391.5 5.9 172.5 5.8 1771 6 372.5 5.8 1771 6 372.5 5.8 1771 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.7 2278 6 382.5 5.7 2278 6 383.5 5.5 5.8 183.5 7 332.5 5.5 1180 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence                             | Sequence                             | Sequence                             | Sequence                                | Sequence         | Sequence         | Sequence         | Sequence          | Sequence         | Sequence         | Sequence         | Sequence            | Sequence            | Sequence          | Sequence          |            |
| 392.5 6.1 784 7 392.5 6.1 392.5 6.1 390.5 6.0 786 7 390.5 6.0 786 7 390.5 6.0 786 7 390.5 6.0 786 7 390.5 6.0 786 7 391.5 5.9 1771 6 372.5 5.8 1771 6 372.5 5.8 1771 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.8 1777 6 372.5 5.7 2278 6 353.5 5.5 5.8 1180 6 332.5 5.5 1180 6 332.5 5.1 835 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | US-11-317-329-12<br>US-11-320-072-96 | US-11-317-329-13<br>US-11-317-329-31 | US-11-317-329-32<br>US-11-317-329-33 | US-10-502-394-94<br>US-10-449-902-54192 | US-10-502-394-93 | US-10-502-334-90 | US-10-570-909-17 | US-10-570-909-107 | US-11-317-329-30 | US-10-502-394-89 | US-10-504-973-30 | US-10-374-780A-1842 | US-11-371-354-61877 | US-10-505-928-177 | US-11-377-316-202 | ALIGNMENTS |
| 392.5<br>392.5<br>392.5<br>392.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>390.5<br>300.5<br>300.5<br>300.5<br>300.5<br>300.5<br>300.5<br>300.5<br>300.5<br>300.5<br>300.5 | ~ ~ !                                | ~ ~                                  | <u>ر</u> ر                           | 9 9                                     | ·ν               | o o              | 9                | 9                 | 7                | 9                | 9                | 9                   | 7                   | 9                 | 7                 |            |
| 392.5<br>3992.5<br>3990.5<br>3990.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5<br>3900.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 784<br>832                           | 786<br>786                           | 786<br>786                           | 1762                                    | 1715             | 1771             | 1777             | 1777              | 347              | 1715             | 1753             | 2278                | 587                 | 1180              | 835               |            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1.0                                  | 0.0                                  | 0.9<br>9.0                           | ເນ<br>ຜູ້                               |                  | , w              | 5.8              | 5.8               | 5.7              | 5.7              | 5.7              | 5.7                 | 5.5                 | 5.5               | 5.1               |            |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 392.5                                | 390.5                                | 390.5                                | 382                                     | 380.5            | 372.5            | 372.5            | 372.5             | 371.5            | 370              | 370              | 368.5               | 357                 | 353.5             | 332.5             |            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 27                                   | 7<br>7<br>8<br>7<br>8                | 30<br>31                             | 32                                      | 8 c              | 36               | 37               | 38                | 39               | 40               | 41               | 42                  | 43                  | 44                | 45                |            |

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APPLICANT: Compugen Ltd
TTLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 1847.1001
CURRENT APPLICATION NUMBER: US/11/050,875
CURRENT APPLICATION NUMBER: 2005-01-27
NUMBER OF SEQ ID NOS: 1583
SEQ ID NO 628
 224
 225 TI------RNTDGRTALDLADPSAKAVLTGEYKKDELLESARSGNEEKMMALLTPLN 275
 210
 276 VNCHASDGRKS------TPLHLAAGYNRVKIVQLLLQHGADVHAKDKG 317
 :| || | | ::|:|:|| | | : | | | 329
 437
 DLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADP 377
 HETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHE 497
 105 ACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDG
 165 GLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEP
 TLINCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQT
 307;
 Length 1880;
 Query Match
13.6%; Score 878.5; DB 7;
Best Local Similarity 25.8%; Pred. No. 1.4e-47;
Matches · 292; Conservative 157; Mismatches 375;
 Sequence 628, Application US/11050875
Publication No. US20060263786A1
GENERAL INFORMATION:
 ; ORGANISM: Homo sapiens
US-11-050-875-628
US-11-050-875-628
 TYPE: PRT
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| 337 HLTPLHVAAHCGHRRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVMELLLKTG 393 498 AKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQ 552   :: :                                                     | Qy 105 ACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDG 164                                                                                                                                           |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                                                                                                                                                                              |                                                                                                                                                                                                                   |
| 631 ENROCHTELOKALELOKAHANVONNANDERK FITELERAAAKKEELCKLELOHGADFIKK 695  [                                                                                                                     | 318 DLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADP :                                                                                                                                                |
| TPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNA                                                                                                                                 | 331                                                                                                                                                                                                               |
| 815 TDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 860  1                                                                                                                                    | Db 338 HLTPLHVAAHCGHHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVMELLLKTG 394  Qy 498 AKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQ 552  Db 395 ASIDAYTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAK 454 |
|                                                                                                                                                                                              | 553<br>455                                                                                                                                                                                                        |
| 849 LDQVVESPAIPRIPCAMPETVVIRSEEQEQASKEYDEDSLIPSPATETSDN 900<br>940 LEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRH 999                                                           | Qy 578 DVETVKKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVP 636                                                                                                                                           |
| 901 ISPVASPVHTGFLVSFM                                                                                                                                                                        | Qy 637 LHNACSYGHYEVABELLVKHGAVVNVADLWK-FTPLHEAAAKGKYEICKLLLQHGADPTKK 695                                                                                                                                          |
| 932 GLRVVIPPRICAAPTRITCRLVKPQKLSTPPPLAEEGGLASRIIALGPIGAQFLSPVIVE 991<br>1035DDKEFQSVEEEMQSTYREHRDGGHAGGIFNRYNILKIQKVCN 1076<br>992 IPHFASHGRGDRELVVLRSENGSVWKEHRSRYGESYLDQILM 1033           | Qy 696 NRDGNTPLDL-VXDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHS 754                                                                                                                                           |
| RESULT 2<br>US-11-050-875-629<br>; Sequence 629, Application US/11050875<br>; Publication No. US20060263786A1                                                                                | Db 670 TPLHLUAQEGH:PVADVLIKHGVMVDATTRAGYTFLHVASHYGNIKLUKFLLQHQADVNA 729  Qy 815 TDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL                                                                                      |
| GENERAL INFORMATION: APPLICANT: Compugen Ltd TITLE OF INVENTION: NOVEL NUCLECTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER | 861                                                                                                                                                                                                               |
| CURRENT PEPLICATION NUMBER: US/11/050,875 CURRENT PILING DATE: 2005-01-27 NUMBER OF SEQ ID NOS: 1583                                                                                         | Qy 885 VLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSGTEGASS 939 ;                                                                                                                                               |
| SEQ ID NO 629 LENGTH: 1881 LYPE: PRT ORGANISM: Homo sapiens                                                                                                                                  | Qy 940 LEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHK 999  1                                                                                                                                        |
| 13.6%; Score 878.5,                                                                                                                                                                          | 1000 LIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSP                                                                                                                                                                          |
| Similarity 25.8%; Pred. No. 1.4e-47;<br>2; Conservative 157; Mismatches 375;                                                                                                                 | Db 933 GLRVVIPPRICAAPTRITCRLVKPQKLSTPPPLAEEGGLASRIIALGFTGAGFLSFVIVE 992 Qy 1035DDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCN 1076                                                                                    |

847

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-----TSLH 679
 740 GYTPLHQAAQQGHTHIINVLLQHGAKPNATTANGNTALAIAKRLGYISVVDTLKVVTEEV 799
 121 EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEV 180
 91 -ANKÄV-------KCAEVIIPLLSSVNVSDRGGRTALHHAALNGHVE 129
 190 SNGQINVVKHLLNLGVEIDEINVYGNTALHIA-----CYN-----GQDAVVN 231
 478 LHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIS 537
 819 AFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL-----VSADDVSALLTAAM
 LAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKW
 : : | :: | : | B00 TTTTTTTTTTEK----HKLAVPETMTEVL-----DVSDEEGDDTMTGDGGEYLRPEDLK
 926 ----SSVVSSSGTEGASSLEKKEVPGVDFSITQFV--RNLGLEHLMDIFEREQITLDVLV
 EDVNTLDS--EKRTPLHVAAFLGDABIIELLILSGARVNAKDNMMLTPLHRAVASRSEA
 181 VNLLLRHGADPNARD-NWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLAD
 240 PSAKAVLTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVK
 360 SKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVT
 420 RIKKHLSLEMVNFKHPQTHE-TALHCAAASPYPKRKQIC-ELLLRKGANINEKTKEFLTP
 873 PPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSEL-----
 300 IVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAA
 | :|:| || |||| || || || || 65 VQVLIKHSADVNARDKNWQ-TPLHVAA-----
 Query Match 11.1%; Score 714.5; DB 7; Length 919; Best Local Similarity 28.7%; Pred. No. 1.6e-37; Matches 246; Conservative 109; Mismatches 287; Indels 215,
642 VTPLHLASQEGHTDMVTLLLDKGANIHMSTKSGL--
 ATTLE OF INVENTION: Novel full length CDNA FILE REFERENCE: H.-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
 980 EMGHKELKEIGINAYGHRHKLIKGVERL 1007
 Sequence 4122, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 RESULT 4
US-11-293-697-4122
 ; UKGANTON: ACMO
 SEQ ID NO 4122
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 440 TALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAK 499
 403 IQAITESGLTPIHVAAFMGHLNIVLLLLQNGASPDVTNIRGETALHMAARAGQVEVVRCL 462
 700 NTPLDLV-KDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLH 758
 ACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHN 384
 74
 193 -NDHNADVOSKMMVNRTTESGFTPLHIAAHYGNVNVATLLLNRGAAVDFTARNGITPLHV
 105 ACRNGDVER-VKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDD
 GGLI PLHNACS FGHABVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCI VLLQHGAE
 PTIRNTDGRT----ALDLADPSAKAVLTGEYKKDEL----LESARSGNEEKMMALLTPLN
 VNCHASDGRKS-----TPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVPLHN
 385 KSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHP----QTHE
 346 TALHVAA---HCGHYRVTKLLLDKRANPNARALNGFTPLHIACKKNRIKVMELLVKYGAS
 ETVKKLCTVQSVNCRDI EGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHN
 ACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDG
 582 AAHYDNOKVALLILERGASPHATAKNGYTPLHIAAKKNOMOIASTLLNYGAETNIVTKQG
 VNALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGN-----ENVQQL
 LQEGI------AAKAGDV
 Query Match
13.6%; Score 877; DB 7; Length 1330;
Best Local Similarity 29.7%; Pred. No. 9.9e-48;
Matches 293; Conservative 137; Mismatches 402; Indels 156; Gaps
 :|| : : |
--SRYGESYLDQILN 1034
 APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108;260
PRIOR PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3237
Sequence 3237, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3237
 US-11-293-697-3237
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143 GRKDVVEYLLQNGANVQARDDGGLIPLHNA----CSFGHAEVVNLLLRHGADPNARDNW 197
 258 SARSGNEEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKG 317
 378 TLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQT 437
 438 HETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHE 497
 678 KYEICKLILIQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKK 737
 738 LSSPDNVNCRDTQCRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYG 797
 798 HVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLK-NQEGQTPL 856
 857 DLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSL--SAASS 914
 ---GGGD-----MQPS-----LRGL--PNGPTHAFSSPSESPDSTVDRQKSS 492
 915 LDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITOFVRNLGLEHLMDIFEREQI 973
 TITLE OF INVENTION: COMPOSITIONS AND METHODSF OR THE TREATMENT OF IMMUNE TITLE OF INVENTION: RELATED DISBASES FILE REFERENCE: P1948R1 US CURRENT APPLICATION NUMBER: US/10/533,519
 354 ------HTCNQGATALCIAAQEGHIDVVQVLLEHGADPNHADQFGRTAMRVAAKNG
 2 GHREIVEHLLDHGAEVNHEDVDGRTALSVAALCVPASKGHASVVSLLIDRGAEVDHCDKD
 198 NYTPLHEAAIKGKIDVCIVLLOHGABPTIRNTDGRTALDLADPSAKAVLTGBYKKDBLLE
 62 GMTPLLVAAYEGHVDVVDLLLEGGAD--VDHTD----------
 -----NNGR--TPLLAAASMGHASVVNTLLFWGAAVDSIDSE
 318 DLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADP
 ------ICEALIEQGARTNEIDNDGRIPFILASQEGHYDCVQILLENK
 498 AKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQE
 ------VNCKDADGRPT--LYILALENQLTMAE
 618 YLLQHGADVHAXDKGGLVPLHNACSYGHYEVAELLVKHGAVNNVADLWKFTPLHEAAAKG
 558 GISLGNSBADROLLBAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVE
 338 HVKVVQLLIEHG-------AVVD------AVVD------
 218 SNIDORGYDGRNALRVAALEGHRDIVELLFSHGAD-------
 -----PEGHRL----
 Sequence 1308, Application US/10533519
Publication No. US20060263774A1
GENERAL INFORMATION:
 APPLICANT: CLARK, HILARY
APPLICANT: SCHOENFELD, JILL
APPLICANT: VANLOOKEREN, MENNO
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
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 US-10-533-519-1308
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 APPLICANT: LIANG, PENG
TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS
TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS
TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS
TITLE OF INVENTION: COLLECTION NUMBER: US/11/371,354
CURRENT APPLICATION NUMBER: US/11/371,354
FRIOR FILING DATE: 2006-04-19
FRIOR FILING DATE: 2006-04-19
FRIOR FILING DATE: 2005-03-05
FRIOR PELICATION NUMBER: 60/665,20
FRIOR PELICATION NUMBER: 60/659,493
FRIOR FILING DATE: 2005-03-07
FRIOR PELICATION NUMBER: 60/659,492
FRIOR PELICATION NUMBER: 60/659,492
FRIOR PELICATION NUMBER: 60/659,492
FRIOR PELICATION NUMBER: 60/659,492
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FRIOR PELICATION NUMBER: 60/659,493
FRIOR PELICATION NUMBER: 60/659,493
FRIOR PELICATION NUMBER: 60/659,493
FRIOR FILING DATE: 2005-02-15
FRIOR FILING DATE: 2005-02-15
FRIOR FILING DATE: 2005-02-15
FRIOR FILING DATE: 2005-02-15
FRIOR FILING DATE: 2005-02-08
NUMBER OF SEQ ID NOS: 78682
SOFTWARE PREACTION VERSION 3.3
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 19;
 709
 -TPLH-ASVINGHTLCLRLLEIADNPRAVDVKDAKGQTPLMLAVAYGHIDAVSLLLEKE 668
 657
 437
 -----KGKYEIC-KLLLQHG 689
 497
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 753
 STPLHLAAGYNNLEVAEYLLQHGAD----VNAQDKGGLIPLHNAASYGHVDVAALLIKYN 809
 538 LOGFTALOMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIE 597
|:|: ::::|
ANPSIRDKEGYNSIHYAAAYGHRQCLELLLERTNSGFEESDSGATKSPLHLAAYNGHHQA
 438 NVNETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEKEATLCLEFLLQND
 ADPTKKNRDG----NTPLDLVK-DG----
 -----DIDIODLLRGDAALLDAAKKGCLARVKKLSSP-----DNVNCRDTQGRH
 810 ACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADD----VS
 GROSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA
 558 LEVLLOSLVÖLDÍRĎ-EKĠRTÁLDLÁÁFKGHTECVEALINPGASIFVKÖNVTKŘ-----
 Gaps
 Query Match 8.2%; Score 527; DB 7; Length 743; Best Local Similarity 24.0%; Pred. No. 1.3e-25; Matches 201; Conservative 98; Mismatches 238; Indels 302;
 345 IHSMPPLHLAALN-----AHSDCCRKLL--SSGFBIDTPDKF----
 ; Sequence 56501, Application US/11371354; Publication No. US20060275794A1; GENERAL INFORMATION:
 866 ALLTAAMPPSALPSCYK 882
 ELLOMAL -- SEEDCCFK 743
 658 VVNVADLWKFTPLHEAAA-
 APPLICANT: CARRINO, JOHN
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-56501
 SEQ ID NO 56501
LENGTH: 743
 285
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TYPE: PRT
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 61 MKTILEGIDPAKHQEHESEGGRTPLMKAARAGHLCTVQFLISKGANVNRATANNDHTVVS 120
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 104 EACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDD 163
 164 ------GGLIPLHNACSFGHAEVVNLLLRHGADPN-ARDNWNYTPLH 203
 -DLADPSA 242
 243 KAVLTGEYKKDELLESARSGNB-----EKMMALLTPLNVN-----CHASDGRKST 287
 288 PLHLAAG-----YNRVKIVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGA 342
 241 TSNVASQSMPPVYPSVDV------DAHTESNHD-TALTLACAGGHEELVSVLIARDA 290
 CVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAY 402
 EFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLR 462
 463 KGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNAL--DNLGQTSLHRAAYCGHL 520
 521 QTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVE 580
 581 TVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNA 640
 ------AQIETNRNTALTLACFOGRAEVVSLLLDRKANVEHRAKTGLTPLMEA 475
 CSYGHYEVAELLVKHGAVVNVADL--WKFTPLHEAAAKGKYBICKLLLQHGADPTKKNRD 698
 | |- || : || :|| :|| :| :|| || 3476 ASGGYAEVGRVLLDKGADVNAPPVPSSRDTALTIAADKGHYKFCELLIHRGAHIDVRNKK 535
 GNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLH 758
 759 LAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIK------ 807
 EASOEGHLELVKYLLA-SGANVHATTATGDTALTYACENGHTDVADVLLQAGADLDKQED
 291 KIEHRDKKGFTPLILAATAGHVGVVEILLDKGGD-------
 Query Match 7.8%; Score 505.5; DB 6; Length 685;
Best Local Similarity 24.0%; Pred. No. 2.8e-24;
Matches 195; Conservative 92; Mismatches 264; Indels 263; Gaps
 --YNACVNATDKWAFTPLHEAAQ---KGRTQLCA 836
 502 MRYIATI--TDKELLKKCHOCVETIVKAKDOOAA 633
 EAAIKGKIDVCIVLLQHGAEPTIRNTDGRTAL-
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: PCT/US03/34312
PRIOR FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/423,394
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 2517
SEQ ID NO 1308
LENGTH: 685
 PAVKLLLDMGSDIN-----
 GNTPLWLASNG------
 ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-519-1308
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APPLICANT: PLOWNAN, GREGORY D.
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WHYNE, DAVID
APPLICANT: WHANING GERAD
APPLICANT: WARTINEZ RICHARD
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE-LIKE
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: 036602/1366
CURRENT APPLICATION NUMBER: US/11/375,615
PRIOR APPLICATION NUMBER: US/10/182,243
PRIOR PLILING DATE: 2003-07-07
PRIOR PLILING DATE: 2001-07-07
PRIOR FILING DATE: 2001-07-07
PRIOR FILING DATE: 2001-07-07
PRIOR FILING DATE: 2001-07-07
PRIOR FILING DATE: 2001-07-07
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 765
 10;
 115 KRLVTPEKVNSRDTA----GRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLH 170
 341 LOLSDRKNLVPRDEELCIYENKVTPLHFLVAQGSVEQVRLLLAHEVDVDCQTASGYTPLL 400
 230
 288
 497
 289 LHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD 348
 557
 349 LWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHS 408
 409 ILQAAREADVTRIKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANIN 468
 ----- 588
 528
 QSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEV 648
 529 YGCDPNIISLQGFTALQMGNENVQQLLQEGISLGNSBADRQLLBAAKAGDVETVKKLCTV 588
 171 NACSFGHAEVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTD
 461 GWTPLHL-------AAONNFENVARLLVSROADPNLHEAEGK--TP
 469 EKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLS
 231 GRTALDLADPSAKAVLTGEYKKDELLESARSGNEEKMMALLT--PLNVNCHASDGRKSTP
 58 LLLRLLALLLAVAAARIMSGRRCAGGGAACASA---AAEAVEPAARELFEACRNGDVERV
 Gaps
 649 AELLUVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLOHGADPTKKNRDGNTP 702
 Query Match 7.4%; Score 478; DB 7; Length 765; Best Local Similarity 24.5%; Pred. No. 1.9e-22; Matches 160; Conservative 79; Mismatches 225; Indels 190;
 SGYGPLHTAAARGKYLICKMLLRYGA-
Sequence 56, Application US/11375615
Publication No. US20060188974A1
GENERAL INFORMATION:
 648 CGADPNAAEQSGW------
 ; ORGANISM: Homo sapiens
US-11-375-615-56
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NUMBER OF SEQ ID NOS: 44
SOFWARE: Patentin version 3.1
SEQ ID NO 34
LENCTH: 765
PRIOR FILING DATE: 2002-04-23
 Best Local Similarity 30.1%
Matches 144; Conservative
 ORGANISM: Homo sapiens
 TYPE: PRT
ORGANISM: Homo sapiens
 US-11-317-329-35
 US-11-317-329-35
 US-11-317-329-34
 SEQ ID NO 35
 Query Match
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 Sequence 34, Application US/11317329
Sequence 34, Application US/11317329
Bublication No. US2006010541341
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Wachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UN-06967
CURRENT FPLING DATE: 2005-12-22
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
 APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06667
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT PILING DATE: 2005-12-22
PRIOR PPLIOR SPPLICANTON NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
 385 KSAIDLAP----TPQLKERLAYEPKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 440
 621 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 680
 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA------HEV 386
 441 ALHCAAASPYPKRKQICELLLRKGANINEKTKEPLTPLHVASEKAHNDVVEVVVKHEAKV 500
 387 DVDCQTASGY-------AGADAGADAGADAGADAGADA 421
 471
 561 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740
 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYL 574
 575 İCKMLLRYGASLELPTHQGWTPLHL--------AAYKGHL-EIIHLLA 613
 614 ESHANMGALGAVNWTPLHLAARHGERAVVSALLQCGADPNAAEQSGWTPLHLAVQRSTFL 673
 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL 858
 NALDNIGOTSLHRAAYCGHLOTCRILLSYGCDPNIISLOGFTALOMGNENVOOLLOEGIS
 Gaps
708 LKVLVEAGAQLDVQDGVSCTPLQLALRSRKQGIMSFL--EGKEPSVATLGGSKP 759
 88;
 7.2%; Score 465; DB 7; Length 765; 30.1%; Pred, No. 1.3e-21; tive 65; Mismatches 181; Indels
 Sequence 3, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
 Query Match
Best Local Similarity 30.1%
Matches 144; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 11-317-329-34
 US-11-317-329-3
 US-11-317-329-3
 501
 422
 681
 472
 SEQ ID NO 3
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Sequence 35, Application US/11317329

Sublication No. US20060105413A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Nuncez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
TITLE OF INVENTION: Momber: US/11/317,329
CURRENT FILING DATE: 2005-12-22
RICH APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ 1D NOS: 44
SOFTWARE: PatentIn version 3.1
 æ
 8
 440
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 385 KSAIDLAP----TPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 440
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 575 ICKMLLRYGASLELPTHQGWTPLHL--------AAYKGHL-EIIHLLA 613
 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGGTPLDL 858
 385 KSAIDLAP----TPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET
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 88;
 7.2%; Score 465; DB 7; Length 765; 30.1%; Pred. No. 1.3e-21; cive 65; Mismatches 181; Indels 8
Length 765,
Query Match 7.2%; Score 465; DB 7; Length 76
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels
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Sequence 37, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Machiro
TILLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-05867
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR PILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
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 -------AAYKGHL-EIIHLLA 613
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 561 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
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 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYL 574
 575 ICKMLLRYGASLELPTHQGWTPLHL--------AAYKGHL-EIIHLLA 613
 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL 858
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 Query Match 7.2%; Score 465; DB 7; Length 765; Best Local Similarity 30.1%; Pred. No. 1.3e-21; Matches 144; Conservative 65; Mismatches 181; Indels
 575 İCKMLLRYGASLELPTHQGWTPLHL-
 ; ORGANISM: Homo sapiens
US-11-317-329-37
 RESULT 12
US-11-317-329-37
 TYPE: PRT
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 Sequence 36, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:
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APPLICATION UNMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR FILING DATE: 2005-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Version 3.1
SEQ ID NO 36
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 441 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 500
 ------TPLLIAAQDQQPDLCALLLAHGADA 421
 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 560
 561 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
 621 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 680
 681 ICKLILOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740
 575 ICKMLLRYGASLELPTHQGWTPLHL--------AAYKGHL-EIIHLLA 613
 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
 385 KSAIDLAP----TPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 440
 387 DVDCQTASGY------AHDINAQDQQPDLCALLLAHGADA 421
 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 560
 561 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 620
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 1.2%; Score 465; DB 7; Length 765; Similarity 30.1%; Pred. No. 1.3e-21; 44; Conservative 65; Mismatches 181; Indels
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 Matches 144; Conservative
 387 DVDĆQTASGY---
 ; TYPE: PRT
; ORGANISM: Homo sapiens
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SOFTWARE: PatentIn version 3.1
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 Sequence 39, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TILLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
PRIOR APPLICATION NUMBER: US/11/317,329
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR PILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
 Sequence 38, Application US/11317329
Publication No. US2006010541341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT APPLICATION NUMBER: US/11/317,329
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: 765
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 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL 858
 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
 Gaps
 88;
 Query Match 7.2%; Score 465; DB 7; Length 765; Best Local Similarity 30.1%; Pred. No. 1.3e-21; Matches 144; Conservative 65; Mismatches 181; Indels
 TYPE: PRT
CRGANISM: Homo sapiens
US-11-317-329-38
 RESULT 13
US-11-317-329-38
 US-11-317-329-39
 422
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APPLICANT: Nunez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Inobara, Nachiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REPERENCE: UM-06567
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT APPLICATION NUMBER: US/11/317,329
PRIOR APPLICATION NUMBER: US/11/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 40
LENGTH: 765
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 387 DVDCQTASGY------TPLLIAAQDQQPDLCALLIAHGADA 421
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 422 NRVDEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPLHLAAQN------
 501 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS
 88; Gaps
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 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDL
 7.2%; Score 465; DB 7; Length 765; 30.1%; Pred. No. 1.3e-21; ive 65; Mismatches 181; Indels
 Length 765;
 Query Match 7.2%; Score 465; DB 7; Length 76 Best Local Similarity 30.1%; Pred. No. 1.3e-21; Matches 144; Conservative 65; Mismatches 181; Indels
 ; Sequence 40, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
 Query Match
Best Local Similarity 30.1%
Matches 144; Conservative
 ORGANISM: Homo sapiens
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US-11-317-329-39
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US-11-317-329-40
SEQ ID NO 39
LENGTH: 765
 TYPE: PRT
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| 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800 |
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| 681 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740 |
| QQRNLRTPLHLAVERGKVRAIQHLLKSGAVPDALDQSGYGPLHTA                        |
| 621 QHGADVHAKDKGGLVPLHNACSYGHYBVAELLVKHGAVVNVADLWKFTPLHBAAAKGKYE 680 |
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| 422 NRVDEDGWAPLHPAAQNGDDRTARLLLDHGACVDAQEREGWTPLHLAAQN 471           |
| 501 NALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 560 |
| 387 DVDCQTASGYTPLLIAAQDQPDLCALLLAHGADA 421                           |
| CAHINDVVE                                                            |

Search completed: December 18, 2006, 18:01:15 Job time : 45.3471 secs

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